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March 1, 2003, 09:11:12 ; Search time 36 Seconds (without alignments) 658.850 Million cell updates/sec
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| SIDS2/goddata/geneseq/geneseqp.emb1/AA199.DAT:
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1 MAAARLCLSLLLLSTCVALL......FSEWGSPHAAVPRELSPLDL 178
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Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

SUMMARIES

			Description	11:10:00:00:00:00:00:00:00:00:00:00:00:0						658 Amino acid sequenc				Rat mancreatic mol
5			Ω	1 6	AAB40	AAY05	AAW76	AAB12	AAY87	AAY53	AAB91	AAU06	AAY53657	AAR12
			DB		77	20	13	21	21	21	22	22	21	2
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,	do	Query	Match	1 0	T 00.0	39.3	19.3	19.3	19.3	19.3	19.3	19.3	18.4	14 4
			Score		704	378.5	186	186	186	186	186	186	177	951
		Result	No.		7	7	m	4	S	9	7	8	6	ç

Baughn MR;

Burford N, Bandman O,

(INCY-) INCYTE GENOMICS INC.

Tang YT, Yue H, Lal P,

Rat neuropeptide P Pancraatic polypep Pancraatic polypep Pancraatic polypep Porcine small inte Peptide YY SEC ID	<u> </u>	Human prepro-neuro Human neuropeptide Human neuropeptide Human neuropeptide	neuro prost prost neuro neuro analo	Seven-pass transme Human NOV7 protein Bordetella pertuss Novel human diagno Porcine small inte Human peptide YY Porcine peptide YY Human peptide YY (im-DNP-His26]-PYY	Porcine peptide YY Human peptide YY
AAY87963 AAB91221 AAB91220 AAR07276 AAB91226	AAASUSUZU AAG75364 AAY53660 AAB91109 AAO06156 AAY43334	AAY23828 AAB35660 AAY57078 AAE07919	AABB5107 AABB5118 AAD18305 AAO18305 AAO18054 AAY92665	AA002196 AAE08586 AAR3275 ABG20464 AAR07277 AAR62050 AAR62040 AAR897740	AAW51800 AAW51801
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112 122 144 154	114 118 20 20	100000	22 23 33 33 33 33 33	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~	444

ALIGNMENTS

Extracellular signaling molecule, EXCS; anti-inflammatory, human; immunosuppressive; cytostatic; neuroprotective; gastrointestinal; virucide; antibacterial; anti-HIV, human immunodeficiency virus; antiinfertility; cerebroprotective; nootropic; antiulcer; antifungal; anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological; Human extracellular signaling molecule (EXCS) (ID 5037143CD1). keratolytic; protozoacide; gene therapy AAB48072 standard; protein; 178 AA 99US-0134949. 99US-0144270. 99US-0146700. 19-MAY-2000; 2000WO-US13975. 99US-0157508 (first entry) WO200070049-A2 19-MAY-1999; 15-JUL-1999; 30-JUL-1999; Homo sapiens 04-OCT-1999; 19-MAR-2001 23-NOV-2000 AAB48072; AAB48072

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The invention provides human extracellular signaling molecules (EXCS) and polymucleotides which identify and encode EXCS. EXCS can be expressed by standard recombinant methodology. The amino acid and nucleic acid sequences of EXCS are useful for diagnosing, treating and preventing infections and gastrointestinal (peptic ulcer, dysphagia, preventing infections and gastrointestinal (peptic ulcer, dysphagia, compare tricks), neurological (e.g. epilepsy, ischemic cerebrovascular disease, stroke), reproductive (infertility, owulatory defects, endometriosis), autoimmune /inflammatory (actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease), and cell proliferative disorders including cancers (of the breast, adrenal gland, bone). They may also be used to treat fatal familial insomnia, model. They may also be used to treat fatal familial insomnia, current disorders (anilatis, leishmania, trypanosoma), viral caused by parasites (malaria, leishmania, trypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus, cappylococcus, bacillus), and fungal (aspergillus, blastomyces, cappulation of EXCS agonists, pharmaceutical compositions, and antibodies may also be used to detect and quantify gene expression in biopsied tissues in which expression of EXCS may be correlated with the disease, to determine presence or excess expression of EXCS. EXCS polymolocotage in moreovery composition, and mitorior required hybridization probes, and to detect differences in gene sequences among normal, carrier probes, and to detect differences in gene sequences among normal, carrier probes, and to detect differences in gene sequences among normal, carrier probes, and to detect differences in gene sequences among normal, carrier cor affected individuals. Antibodies may also be used or individuals. Sequences are presented by probes, and to detect and sequence or excess expre
                                                                                                                                    New human extracellular signaling nucleic acids and polypeptides useful for diagnosing, treating and preventing infections and gastrointestingl, neurological, reproductive, and
                                                                                                                                                                                                                                    autoimmune/inflammatory disorders
   Patterson C;
                                                                                                                                                                                                                                                                                       Claim 1; Page 93; 114pp; English.
Lu DAM,
                                                      WPI; 2001-025021/03
                                                                                       N-PSDB; AAC84308
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Azimzai Y,
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178 AA; Sequence

Gaps 1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60 · 0 Query Match
100.0%; Score 964; DB 22; Length 178;
Best Local Similarity 100.0%; Pred. No. 3e-83;
Matches 178; Conservative 0; Mismatches 0; Indels 0;

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TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPAPSRPALGKTGHLCSTGLDQCALGK 120 1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60

à

MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178 121 d ò

121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178

AAY05276 standard; Protein; 95 AA AAY05276; **XXXXXXXXX**

(first entry) 22-JUN-1999

Pangreatic polypeptide.

Pancreatic polypeptide; neuropeptide; immune response; diagnosis; ulcer;

codiseases by detecting mutations in the pancreatic gene, and can diseases by detecting mutations in the pancreatic gene, and can diseases by detecting mutations in the pancreatic polypeptide invaluate to polypeptide invaluations are diseases associated with pancreatic polypeptides can be used to screen for agonists and antagonists which bind the polypeptide by observing the binding, stimulation or inhibition of pancreatic polypeptide activity, in addition of pancreatic polypeptide activity, in addition to direct administration of antisense sequences and soluble pancreatic polypeptides to treat conditions to pervent expression, or pancreatic polypeptide pancreatic polypeptide pancreatic polypeptide pancreatic polypeptide production, and be used to affect endogenous pancreatic polypeptide production, and immune response are used as vaccines to generate an immunological response. Anti-pancreatic polypeptide antibodies are useful for inducting an immune response to immunicated propugation by affinity chromatography. Diseases diagnosed, prevented or treated include: for intake-related disorders e.g. obesity, anorexia and bulimia; parkinson's disease, acute heart failure; hypotension; hypertension; ulcers; asthma; allergies; benign prostatic hypertrophy; and psychotic and dairium damentia and disorders including anxiety, schizophrenia, manic and control addisorders including anxiety, schizophrenia, and psychotic and control addisorders including anxiety, schizophrenia, manic and control addisorders including anxiety, schizophrenia, and psychotic and control addisorders including anxiety, schizophrenia, and psychotic and control addisorders including anxiety, schizophrenia, and psychotic and control addisported and control and control and disorders and control and c ; This sequence is the pancreatic polypeptide of the invention. The pancreatic polypeptide is a member of the neuropeptide family. Pancreatic polynucleotides and polypeptides are useful for diagnosing susceptibility Parkinson's disease; acute heart failure; hypótension; hypertension; uxinary retention; osteoporosis; angina pectoris; myocardial infarction; asthma; allergy; benign prostatic hypertrophy; psychotic disorder; neurological disorder; cancer. 61 TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPAPSRPALGKTGHLCSTGLDQCALGK 120 1 MAAACRCLSLLLLSTCVALLLQPLLGARGAPLEPLYPGDNTTPEQMAQYTAELRRYINML 60 Gaps 62 121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178 therapy; food intake-related disorder; obesity; anorexia; bulimia; New pancreatic neuropeptide polypeptide and polynucleotide, useful as diagnostic reagents and for prevention and treatment of cancer, 95 1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML ---HRYGERDKEDTLAFSEWGSSHAAVPRELSPLDL 83; delirium, dementia, severe mental retardation and Length 95; Indels 7; Score 378.5; DB Pred. No. 3e-28; 4; Mismatches Claim 10; Page 14-15; 16pp; English. dyskinesias; and cancer and pain. (SMIK) SMITHKLINE BEECHAM PLC. 39.3%; 97EP-0307187. 98EP-0304691. Conservative asthma and schizophrenia WPI; 1999-217067/19. Best Local Similarity Matches 84; Conserv 95 AA; N-PSDB; AAX28413 15-JUN-1998; 16-SEP-1997; Homo sapiens EP908515-A2. Southan CD; depression, Sequence Query Match 63 ---g ð 셤 8 g ð

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Human pancreatic polypeptide.
           20-JUN-2001 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This human pancreatic polypeptide fragment is used in a method for treating non-insulin-dependent diabetes mellitus (NIDDM). The method involves administering a composition comprising pencreatic polypeptide or C-terminal pancreatic polypeptide fragment in a carrier. Screening a composition for the ability to treat NIDDM is also possible and involves determining if the composition decreases hepatic expression of the alpha subunit of a Gs protein in a liver cell plasma membrane, thereby inhibiting stimulation of cyclic adenosine monophosphate (CAMP) by glucagon, determined if the composition blinds the vagal nuclear complex and inhibits secretions of digestive enzymes by the exocrine pancreas, thereby inhibiting beta cell and pancreatic islet hypertrophy or hypothalamus and potentiates the effect of leptin in reducing neuropeptide Y synthesis, thereby enhancing insulin sensitivity and neuropeptide Y synthesis, thereby enhancing insulin sensitivity and
                                                                                                                                               Non-insulin dependent diabetes mellitus; NIDDM; hepatic glucose; pancreatic polypeptide; PP; treatment; Gs protein alpha subunit; inhibitor; cyclic adenosine monophosphate; cAMP; glucagon; secretion; exocrine pancreas; beta cell; pancreatic islet hypertrophy; insulin; neuropeptide Y; hyperglycaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neuropeptide Y synthesis, thereby enhancing insulin sensitivity and reversing the effects of neuropeptide Y. The NIDDM treatment method decreases hyperglycaemia and increases insulin sensitivity without additional detrimental effects.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                     of non-insulin-dependent diabetes mellitus - with
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                                                                                                                           Pancreatic polypeptide fragment for NIDDM treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.3%; Score 186; DB 19;
100.0%; Pred. No. 1.5e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          (UYSC-) UNIV SOUTH CAROLINA MEDICAL RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   pancreatic polypeptide or C-terminal fragment
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                                              AAW76722 standard; peptide; 36 AA.
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                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-609185/51.
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les 35; Conserv
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                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                         26-FEB-1997;
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                                                                         AAW76722;
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                      RESULT 3
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ID AAB1
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AC AAB1
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reproductive system. Why is one of a family of neuropeptides. Other members of the family include peptide YY (PYY, see AABL277), and the present sequence, human pancreatic Polypeptide (HPP). Rat pancreatic polypeptide is described in AABL2180. Selective NPY-Y4 receptor agonists cause an increase in the circulating levels of luteinizing hormone (LH) and hence improve the fertility of animals with compromised reproductive linction. The NPY-Y4 agonists may be used to treat human reproductive disorders such as delayed puberty and amenorthea. In addition, NPY-Y4 antagonists may be used to treat human reproductive disorders such as delayed between the productive disorders such as delayed momerated by preceding the NPY-Y4 and productive disorders such as many preceding preceding profused and hormone-dependent neoplasias e.g. breast cancer and prostate cancer. The present sequence was used in a sequence homology
                              NPY; NPY-Y4 receptor; precocious puberty; pancreatic polypeptide; polycystic ovary syndrome; endometriosis; benign prostatic hyperplasia; delayed puberty; amenorrhea; breast cancer; prostate cancer; PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Human; neuropeptide Y; luteinizing hormone; reproductive system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  puberty, polycystic ovary syndrome and endometriosis, comprises administering a neuropeptide Y \cdot Y A receptor ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuropeptide Y (NPY) (AAB12177) has a number of effects on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.3%; Score 186; DB 21; Length 36; 100.0%; Pred. No. 1.5e-10; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hayward A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY87962 standard; peptide; 36 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98GB-0025969
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                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, pancreatic polypeptide, transplanted pancreatic tissue viability, graft deterioration; immunosupressive treatment, insulin, pancreatic tissue; diabetic; clinical monitor; early transplant viability; transplant survival.
            Neuropeptide; human; treatment; reproductive disorder; neuropeptide Y; endocrine; gynecological; cytostatic; puberty; endometriosis; polycystic ovary syndrome; prostatic hyperplasia; amenorrheae.
                                                                                                                                                                                                                                                                                                                                         Compositions containing a neuropeptide Y Y4 receptor ligand selective for the hyporthalmaic-piuhitary-gonadal axis, for treatment of reproductive disorders e.g. delayed or precocious puberty, endometriosis and benign prostatic hyperplasia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35
                                                                                                                                                                                                                                                                             Broqua P;
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 2; 12pp; English.
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                                                                                                                                                                             98GB-0025969.
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es 35; Conserv
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                                                                                Homo sapiens
                                                                                                                                                                             26-NOV-1998;
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The present sequence represents a human pancreatic polypeptide. The polypeptide is used in the method of the invention, for monitoring transplanted pancreatic tissue viability. The method comprises screening for the modulation of the level of a transplant tissue derived molecule or its derivative, e.g. pancreatic polypeptide, in the body full of the method is useful for monitoring the viability of transplanted pancreatic tissue in a mammal by screening for an increase or decrease in the level of a transplant tissue derived molecule. The method is an indicator of graft damage or deterioration which would permit the commencement of immunosuppressive treatment. The method is especially useful for monitoring the viability of insulin producing foctal pancreatic tissue which has been transplanted into diabetic patients. The method is also useful as an non-invasive clinical monitor of early transplant viability
                                                                                                                        New method for monitoring transplanted pancreatic tissue viability in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protection, endogenous therapeutic peptide, peptidase, conjugation, blood component, modification, succinimidyl, maleimido group, amino, hydroxyl, thiol, hormone, growth factor, neurotransmitter.
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                                                             Duncan MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 36;
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                                                             Bucknall MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.3%; Score 186; DB 21;
100.0%; Pred. No. 1.5e-10;
tive 0; Mismatches 0;
               SOUTHEASTERN SYDNEY AREA HEALTH SERVICE.
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                                                             Brown AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Milner PG,
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                                                                                                                                                                        Disclosure; Fig 7; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                             and on-going transplant survival
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                                                             Amaratunga AP,
                            UNISEARCH LTD.
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Best Local Similarity
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                                                                                           WPI; 2000-053124/04
                                                                                                                                                                                                                                                                                                                                                                                                                                            36 AA;
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15-OCT-1999;
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Sat Mar

SXS

peptidase degradation, useful for increasing length of in vivo activity

Disclosure; Page 325; 733pp; English

The present invention describes a modified therapeutic peptide (I)

comprising a therapeutically active amino acid region (III) and a

reactive group (II) (e.g. succinimidyl and maleimido groups) attached

comprising a therapeutically active amino acid region (IV), which covalently

bonds with amino/hydroxyl/thiol groups on blood components to form a

peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth

in vivo for the treatment of various disorders. Endogenous therapeutic

peptides are not suitable as drug candidates as they require frequent

comprise are not suitable as drug candidates as they require frequent

modifying and attaching therapeutic peptides to albumin prevents or

reduces the action of peptidases to increase length of activity (half

intracellular uptake and interference with physiological processes.

ABB0829 to ABB2441 represent peptides which can be used in the

exemplification of the present invention.

36 AA; Sequence

Gaps ö Length 36; Indels Score 186; DB 22; Pred. No. 1.5e-10; 19.3%; Scor.
100.0%; Pred. No. ...
0; Mismatches Best Local Similarity 100. Matches 35; Conservative Query Match

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1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64 ઠ g

RESULT

AAU06196 standard; peptide; 36 AA AAU06196 XXXXXXXXXX

AAU06196;

04-DEC-2001 (first entry)

Mammalian pancreatic polypeptide (PP).

receptor; Mammalian; brain aluminium concentration; central nervous system; CNS; peptide tyrosine-tyrosine receptor; PYY receptor; PP receptor pancreatic polypeptide receptor; Alzheimer's disease; nootropic; neuro protective

Mammalia

WO200158409-A2

16-AUG-2001.

07-FEB-2001; 2001WO-US03952

08-FEB-2000; 2000US-0499980.

(UYNC-) UNIV NORTH CAROLINA STATE.

Taylor IL;

Croom WJ, Berg BM,

WPI; 2001-550001/61.

Reducing aluminium levels in the central nervous system, for the treatment of Alzheimer's disease comprises administration of a peptide tyrosine receptor agonist or a pancreatic polypeptide receptor agonist

Disclosure; Page 6; 52pp; English.

The present invention relates to a method of reducing aluminium levels

Sequence

ö The present sequence represents a porcine pancreatic polypeptide. The polypeptide is used in the method of the invention, for monitoring transplanted pancreatic tissue viability. The method comprises screening for the modulation of the level of a transplant tissue derived molecule or its derivative, e.g. pancreatic polypeptide, in the body fluid. The method is useful for monitoring the viability of transplanted pancreatic tissue in a mammal by screening for an increase or decrease in the level of a transplant tissue derived molecule. The method is an indicator of graft damage or deterioration which would permit the commencement of immunosuppressive treatment. The method is especially useful for monitoring the viability of insulin producing foetal pancreatic tissue which has been transplanted into diabetic patients. The method is also useful as an non-invasive clinical monitor of early transplant viability and on-going transplant survival. Pig; pancreatic polypeptide; transplanted pancreatic tissue viability; graft damage; graft deterioration; immunosuppressive treatment; insulin; pancreatic tissue; diabetic; clinical monitor; early transplant viability; transplant survival. comprises administration of a peptide tyrosine-tyrosine (PYY) receptor agonist or a pancreatic polypeptide (PP) receptor agonist. The method is useful for the treatment of Alzhaimer's disease and for reducing aluminium levels in the central nervous system, especially the brain, of a subject. The treatments are effective and do not impart excessive toxicological effects. The present sequence represents mammalian pancreatic PP. New method for monitoring transplanted pancreatic tissue viability in Gaps ö Duncan MW; Length 36; Amino acid sequence of the porcine pancreatic polypeptide. Indels Bucknall MP, 19.3%; Score 186; DB 22; 100.0%; Pred. No. 1.5e-10; iive 0; Mismatches 0; The method (SESY-) SOUTHEASTERN SYDNEY AREA HEALTH SERVICE. (UNIX) UNISEARCH LTD. 64 1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR central nervous system (CNS). Brown AS, Ä. Disclosure, Fig 7; 70pp; English. AAY53657 standard; protein; 36 99WO-AU00361. 98AU-0003490. 22-FEB-2000 (first entry) Conservative Amaratunga AP, WPI; 2000-053124/04. Local Similarity es 35; Conserv 36 AA; 36 AA 13-MAY-1999; WO9958979-A1 13-MAY-1998; 18-NOV-1999. AAY53657; Sequence Tuch BE, Query Match Sus sp. Matches RESULT 9 AAY53657 888888888 ð g

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropeptide Y (NPY) (AAB12177) has a number of effects on the reproductive system. NPY is one of a family of neuropeptides. Other members of the family include peptide YY (PYY, see AAB12177), and the present sequence, rat pencreatic polypeptide (RPP). Human pancreatic polypeptide is described in AAB12179. Selective NPY-Y4 receptor agonists have been found (see AAB12181 to AAB12183). The NPY-Y4 receptor agonists cause an increase in the circulating levels of luteinizing hormone (LH) function. The NPY-Y4 agonists may be used to treat human reproductive disorders such as delayed puberty and amenorhea. In addition, NPY-Y4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer. The present sequence was used in a sequence homology
                                                                                                                                                                                                                                                                                                     Rat; neuropeptide Y; luteinizing hormone; reproductive system; NPY; NPY-Y4 receptor; precocious puberty; pancreatic polypeptide; polycystic ovary syndrome; endometriosis; benign prostatic hyperplasia; delayed puberty; amenorrhea; breast cancer; prostate cancer; PP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antagonists may be used to treat human reproductive disorders such as precocious puberty, endometriosis, polycystic ovary syndrome, benign prostatic hyperplasia and hormone-dependent neoplasias e.g. breast can
                                     Gaps
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Length 36;
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                                  Indels
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1.1e-09;
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18.4%; Score 177; DB 21; 94.3%; Pred. No. 1.1e-09;
                                                           30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
                                                                              1 APLEPVYPGDDATPEQMAQYAAELRRYINMLTRPR 35
                                2; Mismatches
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               Similarity
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neuropeptide Y (NPY) Y4 receptor ligand for treatment of human reproductive disorders. The products described in the invention have endocrine, gynecological and cytostatic activity and can be used for the treatment of reduced reproductive function, delayed puberty, supranormal function of the reproductive function, precocious puberty, endometriosis, polycystic ovary syndrome, benign protestic hyperplasia, impaired reproductive function or amenorrheae. This sequence represents the rat PP neuropeptide which is used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions containing a neuropeptide Y Y4 receptor ligand selective for the hypothalamic-pituitary-gonadal axis, for treatment of reproductive disorders e.g. delayed or precocious puberty, endometriosis and benign prostatic hyperplasia -
                                                                                                                                                                                                                  Neuropeptide; rat; treatment; reproductive disorder; neuropeptide Y; endocrine; gynecological; cytostatic; puberty; endometriosis; polycystic ovary syndrome; prostatic hyperplasia; amenoriheae.
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Synthetic.

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The present invention describes a modified therapeutic peptide (1) comprising a therapeutically active amino acid region (III) and a reactive group (II) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3.50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as draig candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases. AMB90829 to AMB9241 represent invention.
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Protection; endogenous therapeutic peptide; peptidase; conjugation; blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 327; 733pp; English.
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99US-0159783.
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Matches 27; Conservative
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15-OCT-1999;
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                                                                     Homo sapiens
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                                                                                     Synthetic.
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The present invention describes a modified therapeutic peptide (1) comprising a therapeutically active amino acid region (III) and a reactive group (III) (e.g. succinimidyl and maleimido groups) attached to a less therapeutically active amino acid region (IV), which covalently bonds with amino/hydroxyl/thiol groups on blood components to form a peptidase stabilised therapeutic peptide composed of 3-50 amino acids. (I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disconders. Bndogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body
                                                                                                                                                                                                                                                                                      Modifying and attaching therapeutic peptides to albumin prevents peptidase degradation, useful for increasing length of in vivo activity
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                                                                                                                         99US-0134406.
99US-0153406.
99US-0159783.
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Best Local Similarity
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                              WO200069900-A2
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10-SEP-1999;
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                                                                                                                                                                               The analogue also has improved internal-secretion inducing and nervetropic activities. These include bradycardia, vasoconstriction and acceleration of feeding behaviour. The analogue also inhibits smooth muscle contraction in the ductus deferens and the uterus caused by electrical stimuli. See also AAR07277 and AAR07278.
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protection, endogenous therapeutic peptide; peptidase; conjugation, blood component; modification; succinimidyl; maleimido group; amino; hydroxyl; thiol; hormone; growth factor; neurotransmitter.
                                                                                                                                                      synthetic analogue is derived from porcine peptide YY. It has N-
                                                                                                                                                                     terminal substitutions which render the core structure more stable.
                                                                                 N-terminal analogue peptide(s) of porcine upper small intestine having improved central and peripheral nerve-tropic actions
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                                                                                                                                                                                                                                                                                              11.4%; Score 110; DB 11; Length 36; 50.0%; Pred. No. 0.0023; tive 11; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB91226 standard; Peptide; 36 AA
                                                                                                                          Claim 4; Page 1; 15pp; Japanese
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Matches 17; Conservative
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                          (SUNR ) SUNTORY LID.
                                                      WPI; 1990-316711/42.
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27-FEB-1989;
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10-SEP-1999;
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peptidase stabilised therapeutic peptide composed of 3-50 amino acids.

(I) are useful for modifying therapeutic peptides e.g. hormones, growth factors and neurotransmitters, to protect them from peptidase activity in vivo for the treatment of various disorders. Endogenous therapeutic peptides are not suitable as drug candidates as they require frequent administration due to rapid degradation by peptidases in the body. Modifying and attaching therapeutic peptides to albumin prevents or reduces the action of peptidases to increase length of activity (half life) and specificity as bonding to large molecules decreases intracellular uptake and interference with physiological processes. AAB90829 to AAB9241 represent peptides which can be used in the exemplification of the present invention.
with amino/hydroxyl/thiol groups on blood components to form a
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36 AA;

Gaps ; 0 11.4%; Score 110; DB 22; Length 36; larity 52.9%; Pred. No. 0.0023; Conservative 10; Mismatches 6; Indels 9 Local Similarity Les 18; Conserva

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Search completed: March 1, 2003, 09:12:41 Job time : 38 secs

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ALIGNMENTS

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US-09-965-528-16

Sequence 16, Application US/09965528

Publication No. US20020187523A1

GENERAL INFORMATION:

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: INCYTE GENOMICS, INC.

APPLICANT: BANDMAN, Olga

APPLICANT: APITEREORO, Chandra

ITILE OF INVENTION: EXTRACELLULAR SIGNALING MOLECULES

FILE REFERENCE: PF-0701 USA

CURRENT APPLICATION NUMBER: 60/134,949

PRIOR PELING DATE: 1999-05-19

PRIOR PELING DATE: 1999-05-19

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-10-04

SOFTWARE: PERL PROGRAM

SOFTWARE: PRIOR FILING DATE: 1999-10-04

SOFTWARE: PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-07-30

PRIOR FILING DATE: 1999-10-04

SOFTWARE: PRIOR FILING DATE: 1999-07-30

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APPLICANT: Shimkets, Richard A.
APPLICANT: Muralidhara, Padigaru
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 97;
                                                                       Query Match 19.3%; Score 186; DB 12; Length 36; Best Local Similarity 100.0%; Pred. No. 3.1e-09; Matches 35; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10002048A; Publication No. US20020182616A1; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wahlestedt, Claes
JAPLICANT: Wahlestedt, Claes
CITILE OF INVENTION: Single Nucleotide Polymorphisms
CURRENT PELICATION NUMBER: US/10/002,048A; CURRENT FILING DATE: 2001-11-02; PRIOR APPLICATION NUMBER: SE 0004035-2; PRIOR FILING DATE: 2000-11-03; NUMBER OF SEQ ID NOS: 6; SOFTWARE: Patentin version 3.1; SEQ ID NO. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 10.7%; Score 103.5; DB 9; Best Local Similarity 39.1%; Pred. No. 0.056; Matches 25; Conservative 12; Mismatches 18;
                                                                                                                                                                                                            1 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 35
                                                                                                                                                                              30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
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CURRENT APPLICATION NUMBER: US/09/737,149
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR FILING DATE: 1999-12-14
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR PELING DATE: 1999-12-27
PRIOR PELING DATE: 1999-12-27
PRIOR PELING DATE: 2000-01-04
PRIOR APPLICATION NUMBER: 60/174,964
PRIOR APPLICATION NUMBER: 60/174,962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09737149 Patent No. US20020077466A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Spaderna, Steven K APPLICANT: Quinn, Kerry E.
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRPR 64
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       ; ORGANISM: HC
US-10-016-969-1
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APPLICANT: Pittner, Richard
APPLICANT: Pittner, Richard
APPLICANT: Pittner, Richard
APPLICANT: Poung, Andrew
APPLICANT: Paterniti, James
TITLE OF INVENTION: Peptide YY and Peptide YY Agonists for the Treatment of Metabolic
TITLE OF INVENTION: Disorders
TITLE REFERENCE: 24001-010
CURRENT APPLICATION NUMBER: US/10/016,969
PRIOR FILING DATE: 2000-12-14
PRIOR FILING DATE: 2000-12-15
                                                                                                  TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPAPAPALGKTGHLCSTGLDOCALGK 120
                                                                                                                                 TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPAPSRPALGKTGHLCSTGLDQCALGK 120
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1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                             1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
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                                                                                                                                                                                                    MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178
                                                                                                                                                                                                                                      121 MVPTGRYETGGLAPGHSACPCGLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178
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                                                                                                                                                                                                                                                                                                                                                                                                                     ; GENERAL INFORMATION:
APPLICANT: SOUTHAN, CHRISTOPHER
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30015-C1
CURRENT APPLICATION NUMBER: US/09/757,712
CURRENT FILING DATE: 2001-01-10
FRIOR PELLORION NUMBER: EP 97307187.1
FRIOR PELLORION NUMBER: EP 97307187.1
FRIOR APPLICATION NUMBER: 09/110,715
FRIOR FILING DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 2
SOFTHARE: FASTERE OF Windows Version 3.0
SSEC ID NO 2
LENGTH: 95
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Patent No. US20010016339A1
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Patent No. US20020141985A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.0
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ORGANISM: HOMO SAPIENS
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Best Local Similarity
Matches 84; Conserv
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US-09-757-712-2
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LENGTH: 36
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Nicolas, Pierre
TITLE OF INVENTION: PEPTHE IMMUNE SYSTEM IN HUMANS AND ANIMALS
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OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: 02-Jan-2002
                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3909-0021-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.043;
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CORRESPONDENCE ADDRESSE:
Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/181,941
FILING DATE: 28-Oct.-1998
APPLICATION NUMBER: US 08/574,701
FILING DATE: 19-DEC-1995
APPLICATION NUMBER: ER 95 07831
FILING DATE: 29-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.3%; Score 99; DB 47.1%; Pred. No. 0.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/038,045 FILING DATE: 02-Jan-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: No. US20020150964Ale
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10038045; Patent No. US20020150964A1; GENERAL INFORMATION:
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LENGTH: 36 amino acids
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ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION
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Best Local Similarity 47.1%
Matches 16; Conservative
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                                            COUNTRY: USA
ZIP: 10036-2811
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  CITY: New York
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APPLICANT: Young, Andrew
APPLICANT: Young, Andrew
APPLICANT: Paterniti, James
TITLE OF INVENTION: Peptide YY and Peptide YY Agonists for the Treatment of Metabolic
TITLE OF INVENTION: Disorders
FILE REFERENCE: 24001-010
CURRENT APPLICATION NUMBER: US/10/016,969
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/256,216
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                         Length 3014;
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                                                                                                                                                                                                    Score 102; DB 10;
Pred. No. 3.7;
9; Mismatches 63;
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STREET: 1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mor, Amram
Vouldoukis, Ioannis
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Patent No. US20020150964A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-016-969-2
; Sequence 2, Application US/10016969
; Patent No. US20020141985A1
; GENERAL INFORMATION:
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ilarity 29.3%;
Conservative 9
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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CORRESPONDENCE ADDRESS:
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ORGANISM: Homo sapiens
                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Matches 49; Conserv
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                                                                                               LENGTH: 3014
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US-10-038-045-4
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LENGTH: 36
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TELECOMMUNICATION INFORMATION
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US-10-078-650-14
Sequence 14, Application US/10078650
Fatent No. US20020169301A1
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%
Matches 17, Conservative
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US-10-057-136-20
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US-10-057-136-20
                                                                                                                                                                                                                                           US-10-038-045-1
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Nicolas, Pierre
TITLE OF INVENTION: PEFTIDES FOR THE ACTIVATION
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSED for Windows
SOFTWARE: FastSED for Windows
Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/038,045
FILING DATE: 02-Jan-2002
CLASSIPICATION: CUNKNOWN>
PRIOR APPLICATION OF CUNKNOWN>
APPLICATION NUMBER: US/09/181,941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                     NAME: COLUZZI, LAULTA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3909-0021-999
TELECOMMUNICATION INFORMATION:
TELERAX: 650-493-5556
TELERX: 66141 PENNIE
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 3909-0021-999
          PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/181,941
FILING DATE: 28-Oct-1998
APPLICATION NUMBER: US 08/574,701
FILING DATE: 19-DEC-1995
APPLICATION NUMBER: FR 95 07831
FILING DATE: 29-UNN-1995
ATTORNEY AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PPKPENPGEDASPEEMTKYLTALRHYINLVTRQR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
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APPLICATION NUMBER: US 08/574,701
FILING DATE: 19-DEC-1995
APPLICATION NUMBER: FR 95 07831
FILING DATE: 29-UIN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: No. US20020150964Ale
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.0%; Score 96; 50.0%; Pred. No.
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10038045
Patent No. US20020150964A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amram
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Matches
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APPLICANT: KANTOR, JUDITAL
APPLICANT: KANTOR, JUDITAL
APPLICANT: KANTOR, JUDIAL
APPLICANT: KANTOR, JUDIAL
APPLICANT: ALINDA
TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
TITLE OF INVENTION: TUMOR-ASSOCIATED ANTIGEN
FILE REFERENCE: 700953/47113C
CURRENT APPLICATION NUMBER: US/10/057,136
CURRENT APPLICATION NUMBER: 09/366,670
PRIOR APPLICATION NUMBER: 09/366,670
PRIOR APPLICATION NUMBER: 09/366,670
PRIOR PILING DATE: 1999-08-03
PRIOR FILING DATE: 1999-02-24
PRIOR FILING DATE: 1998-0.2-24
PRIOR FILING DATE: 1998-0.2-24
PRIOR FILING DATE: 1998-0.2-24
SPRIOR FILING DATE: 1998-0.2-24
SPRIOR FILING DATE: 1998-0.2-24
SPRIOR FILING DATE: 1907-0.2-24
SOFTWARE: PALCATION NUMBER: 00/38,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 94; DB ]; Pred. No. 0.11; 8; Mismatches
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Pred. No. 2.5;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: No. US20020150964Ale
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81 PAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/10057136
Publication No. US20030021770A1
GENERAL INFORMATION:
APPLICANT: SCHLOM, JEFFREY
TELEPHONE: 650-493-4935
TELEFAX: 650-493-5556
                                                                                                                                                             LENGTH: 36 amino acids
                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                      TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                         9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 27.7%;
Matches 38; Conservative
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Sequence 3. Application US/10016969

Sequence 3. Application US/10016969

Sequence 3. Application US/10016969

Sequence 3. Application US/20020141985A1

GENERAL INFORMATION:

APPLICANT: Amylin Pharmaceuticals, Inc.

APPLICANT: Pittner, Richard

APPLICANT: Young, Andrew

APPLICANT: Young, Andrew

APPLICANT: Poung, Andrew

APPLICANT: Poung, Andrew

TITLE OF INVENTION: Peptide YY and Peptide YY Agonists for the Treatment of Metabolic

TITLE OF INVENTION: Disorders

TITLE OF INVENTION: Disorders

TITLE OF INVENTION: Disorders

TITLE OF INVENTION: Disorders

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: US 60/256,216

PRIOR PELLING DATE: 2000-12-15

NUMBER OF SEQ ID NOS: 6

SEQ ID NO 3

SEQ ID NO 3

LENGTH: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14

US-10-016-969-4

Sequence 4, Application US/10016969

Sequence 4, Application US/10016969

Patent No. US20020141985A1

GENERAL INFORMATION:

APPLICANT: Puttner, Richard

APPLICANT: Pittner, Richard

APPLICANT: Paterniti, James

TITLE OF INVENTION: Paptide YY and Peptide YY Agonists for the Treatment of Metabolic

TITLE OF INVENTION: Disorders

FILE REFERENCE: 24001-010

CURRENT APPLICATION NUMBER: US/10/016,969

CURRENT FILING DATE: 2001-12-14

PRIOR APPLICATION NUMBER: US 60/256,216

PRIOR APPLICATION NUMBER: US 60/256,216

SEQUENCE: PatentIn version 3.0

SEQUENCE: SEQUENCE: PatentIn version 3.0

SEQUENCE: PatentIn version 3.0
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0.15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IKPEAPGEDASPEELNRYYASLRHYLNLVTRQR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 9.2%; Score 89; 1 Similarity 50.0%; Pred. No. (17; Conservative 7; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.5%; Score 92;
45.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 LEPVYPGDNATPEQMAQYAADLRRYINMLTRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 3, Application US/10038045; Patent No. US20020150964A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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US-10-038-045-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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APPLICANT: Bandad, R. Shoshana
APPLICANT: Bandad, R. Shoshana
APPLICANT: Bandad, R. Shoshana
TITLE OF INVENTION: DIAGNOSTIC TUMOR MARKERS, DRUG SCREENING FOR TUMORIGENESIS INHIBI
TITLE OF INVENTION: AND COMPOSITIONS AND METHODS FOR TREATMENT OF CANCER
FILE REPERENCE: M01015/70071
CURRENT APPLICATION NUMBER: US/09/996,069
CURRENT PILING DATE: 2001-11-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AAARLCLSLILLSTCVALLLQPLLGAQG-----APLEPVYPGDNATPEOMAQYAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.6%; Score 93; DB 9; Length 410;
ilarity 29.9%; Pred. No. 2.1;
Conservative 6; Mismatches 53; Indels
APPLICANT: Fujimoto, Katsumi, APPLICANT: Shin, Mei
APPLICANT: Shin, Mei
APPLICANT: Kato, Yukio
TITLE OF INVENTION: NOVEL bill TYPE TRANSCRIPTION FACTOR
TITLE OF INVENTION: GENES DEC2
FILE REFERENCE: 06501-101001
CURRENT APPLICATION NUMBER: US/10/078,650
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US/10/03991
PRIOR PILING DATE: 2000-06-19
PRIOR PILING DATE: 1999-08-19
RIOR PILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 DLRRYINMLTRP-----RCVPQLGREIPAPGTLGPLHIPGHTLSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
9.6%; Score 92.5; DB 9;
Best Local Similarity 27.1%; Pred. No. 8.3;
Matches 42; Conservative 8; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 VPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            832 APPAHGVTS--APDTRPAPGSTAPPAHGVTSAPDT 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          734 PAHGVTSAPDTRPAPGSTAPPAHGVTSAPDTR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 10, Application US/09996069; Publication No. US20030036199A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1255
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 38; Conserv
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US-09-996-069-10
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                                         Nicolas, Pierre
TITLE OF INVENTION: PEPTIDES FOR THE ACTIVATION
OF THE IMMUNE SYSTEM IN HUMANS AND ANIMALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.2%; Score 89; DB 12; Length 36; Best Local Similarity 50.0%; Pred. No. 0.28; Matches 17; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                 MEDLUM TYRE: LUBKECTE COMPUTER: IBM Compatible COPERATING SYSTEM: Windows SOFTWARE: FASESE OF Windows SOFTWARE: FASESE OF Windows CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/038,045
FILING DATE: 02-Jan-2002
CLASSIFCATION OATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/181,941
FILING DATE: 28-OCt-1998
APPLICATION NUMBER: US 08/574,701
FILING DATE: 19-DEC-1995
APPLICATION NUMBER: FR 95 07831
FILING DATE: 29-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELECOMMUNICATION INFORMATION:
                                                                                                                        NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-291
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear

MOLECULE TYPE: No. US20020150964Ale

SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-038-045-3
                               Vouldoukis, Ioannis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 650-493-4935
TELEPAX: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acids
STRANDEDNESS: single
APPLICANT: Mor, Amram
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2 PSKPDNPGEDAPAEDMAKYYSALRHYINLITRQR 35 g

31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64

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Search completed: March 1, 2003, 09:17:19 Job time : 16 secs

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March 1, 2003, 09:11:46; Search time 143 Seconds (without alignments) 802.535 Million cell updates/sec
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2: (cgn2_6/ptodata/1/paa/US06_COMB.pep:*
4: (cgn2_6/ptodata/1/paa/US06_COMB.pep:*
5: (cgn2_6/ptodata/1/paa/US08_COMB.pep:*
6: (cgn2_6/ptodata/1/paa/US081_COMB.pep:*
7: (cgn2_6/ptodata/1/paa/US081_COMB.pep:*
7: (cgn2_6/ptodata/1/paa/US081_COMB.pep:*
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13: (cgn2_6/ptodata/1/paa/US096_COMB.pep:*
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15: (cgn2_6/ptodata/1/paa/US096_COMB.pep:*
16: (cgn2_6/ptodata/1/paa/US096_COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4569144 segs, 644733110 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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964
                              Copyright
                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

				4 :	Appl	Appl	Appli	Appl	App	Appli
			_	!	16,	16.	9	86,	982	0
			Description		Sequence	Segmence	Sequence	Seguence 86, Appl	Sequence	Segmence
COMMAKIES			ID	********	US-09-965-528-16	US-09-979-300-16	US-60-144-270-6	US-10-177-488-86	US-60-200-109-982	US-09-110-715-2
			8		23	23	27	25	27	15
		Query	Length	1	178	178	178	95	87	95
	ф	Query	Match	•	100.0	100.0		45.8		
			Score		964	964	964	441.5	379	378.5
		Result	No.		Н	7	٣	4	S	9

Sequence 2, Appli Sequence 32, Appl Sequence 4961, App Sequence 2397, App Sequence 23, Appl Sequence 112, Appl Sequence 112, Appl Sequence 112, Appl Sequence 28, Appl Sequence 28, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 31, Appl Sequence 6138, Appl Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli	
US-09-757-712-2 US-10-036-657-32 US-60-196-718-4967 US-60-196-718-4967 US-60-192-739-3334 PCT-USO2-30533-25 US-09-657-276-391 US-10-197-2981-112 US-10-197-2981-112 US-10-197-2981-112 US-10-197-2981-112 US-10-197-2981-112 US-10-197-2981-112 US-10-197-2981-112 US-60-196-718-4968 PCT-USO2-30533-29 US-60-196-718-4968 PCT-USO2-30533-33 US-60-195-0533-13 US-60-195-0533-13 US-09-657-276-394 US-09-657-276-394 US-09-657-276-283 US-09-67-276-283 US-09-67-276-283 US-09-708-3444-7	ALIGNMENTS 1965528 INC. SACTOR SIGNALING MOLECULES 15/09/965,528 1144,270 1144,270 1146,700 1157,508
24 27 27 27 27 27 27 27 27 27 27 27 27 27	ILCS, INC mm in lina m. in lina m. ina m.
U T T T T T T T T T T T T T T T T T T T	ication US/ ON: E GENOMICS, Y: Tom Henry Preeti OND, Neil MAN, Olga MAN, Olga ENDOM Ania ENDOM CAN ENDOM CAN ENTRACE PF-0701 USA ION NUMBER: E: 1999-07- E: 1999-07- N NUMBER: E: 1999-07- N NUMBER:
0.000000000000000000000000000000000000	8-16 FORMATION: INCYTE GENOMICS, TANG, Y. Tom TANG, Y. Tom TUE, Preeti BURFORD, Neil BAUDMAN, Olgan BAUGHN, Olgan BAIMZAI, Yalda I, U, DYUNG Alna I PATTERSON CHANA ILU, DYNOR ALNA BAIMZAI, YALGA FELICATION NUMBER: FLICATION NUMB
378.5 378.5 378.5 310.5 310.5 310.5 186 182 182 182 182 183 183 184 187 187 188 188 188 188 188 188 188 188	-528- e 16, ANT: ANT: ANT: ANT: ANT: ANT: ANT: ANT:
7 8 9 9 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RESULT 1 US-09-965-528 Sequence 16 GENERAL INI APPLICANT

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Remaining Prior Application data removed - See File Wrapper or PALM.
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PRIOR APPLICATION NUMBER: US 60/299,500
PRIOR FILING DATE: 2001-06-20
PRIOR PELICATION NUMBER: US 60/300,880
PRIOR PELING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR PILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-39
PRIOR APPLICATION NUMBER: US 60/312,312
PRIOR PILING DATE: 2001-08-13
PRIOR PILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-13
PRIOR PILING DATE: 2001-08-13
PRIOR FILING DATE: 2001-08-14
PRIOR APPLICATION NUMBER: US 60/319,227
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-08-20
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2001-09-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2001-11-07
APPLICATION NUMBER: US 60/378,885
FILING DATE: 2002-05-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Treatment of Tumor FILE REFERENCE: P5001R1 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 86, Application US/10177488 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spencer Susan D.
Smith, Victoria
Williams, P. Mickey
Wu, Thomas D.
FILE REFERENCE: PF-0720 P
CURRENT APPLICATION NUMBER: US/6
CURRENT FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koeppen, Hartmut
Phillips, Heidi S.
Polakis, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Frantz, Gretchen
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 178; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cairns, Belinda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen, Ruihuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-177-488-86
                                                                                                                                   SEQ ID NO 6
LENGTH: 178
                                                                                                                                                                                                                                                                                                                        US-60-144-270-6
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                           1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
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                                                                                                                                                                                                                     Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
TITLE OF INVENTION: Extracellular Signaling Molecules
FILE REFERENCE: [list docket ID here]
CURRENT APPLICATION NUMBER: US/09/979,300
CURRENT FILING DATE: 2001-11-19
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PERL Program
SEQ ID NO 16
LENGTH: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Lal, Preeti
APPLICANT: Baughin, Mariah R.
APPLICANT: Azimzai, Yalda
TITLE OF IMVENTION: EXTRACELLULAR SIGNALING MOLECULES
                                                                                                                                                                                                                100.0%; Score 964; DB 23;
100.0%; Pred. No. 5.2e-73;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 5037143CD1
US-09-979-300-16
                                                                                                          NAME/KEY: misc feature
CTHER INFORMATION: Incyte ID No: 5037143CD1
US-09-965-528-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-979-300-16; Sequence 16, Application US/09979300; GENERAL INFORMATION:
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                                                                                                                                                                                                             Query Match : 100.0
Best Local Similarity 100.0
Matches 178; Conservative
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Best Local Similarity 100.
Matches 178; Conservative
                                TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
        LENGTH: 178
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61 TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPAPARPALGKTGHLCSTGLDQCALGK 120
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                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                             1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Compositions and Methods for the Diagnosis and TITLE OF INVENTION: Treatment of Tumor
                                                                                                                                                                                                                     100.0%; Score 964; DB 27; Length 178; 100.0%; Pred. No. 5.2e-73; ive 0; Mismatches 0; Indels 0
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OAMS/FERS: misc_feature
OTHER INFORMATION: Incyte Clone No: 5037143
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61 TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPAPSRPALGKTGHLCSTGLDQCALGK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----HRYGERDKEDTLAFSEWGSSHAAVPRELSPLDL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 39.3%; Score 378.5; DB 15; Length 95; Best Local Similarity 47.2%; Pred. No. 6.7e-24; Antches 84; Conservative 4; Mismatches 7; Indels 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.3%; Score 378.5; DB 21; Length 95; 47.2%; Pred. No. 6.7e-24; Live 4; Mismatches 7; Indels 83
                    COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FRACESC for Windows Version 2.0
SOFTWARE: FRACESC for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: EP 97307187.1
FILING DATE: 16-SEP-1997
FILING DATE: 16-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESENCE/DOCKET NUMBER: 23 031
REGISTRATION NUMBER: 23 031
REFERENCE/DOCKET NUMBER: GP-30015
TELEFRONE: 610-407-0701
TELEEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TUBERT AMINO ACIDS
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SOUTHAN: CHRISTOPHER
FILLE REFERENCE: GP-30015-C1
CURRENT APPLICATION: NUMBER: US/09/757,712
CURRENT PILING DATE: 2001-01-10
FRIOR APPLICATION NUMBER: EP 97307187.1
FRIOR FILING DATE: 1997-09-16
FRIOR FILING DATE: 1998-07-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FREESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-09-110-715-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
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US-09-757-712-2
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TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Beasley. Ellen
APPLICANT: Beasley. Ellen
TITLE OF INVENTION: USGLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLO000448
CURRENT APPLICATION NUMBER: US/60/200,109
CURRENT FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 1348
SOFTWARE: FEASLEG for Windows Version 4.0
SEQ ID NO 982
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                                                                                                                                                                                                                                                    DB 25; Length 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.3%; Score 379; DB 27; Length 87; 50.3%; Pred. No. 5.5e-24; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PRYGKRHKEDTLAFS-GGSPHAAVPR 87
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                 Score 441.5; DB 25;
Pred. No. 3.2e-29;
0; Mismatches 0;
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Sequence 2, Application US/09110715

GENERAL INFORMATION:

APPLICANT: SOUTHAN, CHRISTOPHER;

TITLE OF INVENTION: NOVEL COMPOUNDS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Rainer & Prestia

STREET: P.O. Box 980

CITY: Valley Forge

STREET: PA

COUNTRY: USA
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.4%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86; Conservative
NUMBER OF SEQ ID NOS: 154
SEQ ID NO 86
1.RNGTH: 95
                                                                                                                                                        ; ORGANISM: Homo Sapien
US-10-177-488-86
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Matches 86; Conserv
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; ORGANISM: HUMAN
US-60-200-109-982
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                                                                                                                                 TYPE: PRT
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Query Match
Best Local Similarity 96.93
Matches 62; Conservative
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC AÇID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL000484
CURRENT PEPLICATION NUMBER: US/60/200,109
CURRENT FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 1348
SOFTWARE: FastSEQ for Windows Version 4.0
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                                61 TRPRCVPQLGREIPAAPGTLGPLHIPGHTLSPAPAPARPARALGKTGHLCSTGLDQCALGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPAPARPALGKTGHLCSTGLDQCALGK 120
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 1 MAAACRCLSLLLLSTCVALLLQPLLGARGAPLEPLYPGDNTTPEQMAQYTAELRRYINML 60
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                                                                                                  121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPLDL 178
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                                                                                                                                      -----HRYGERDKEDTLAFSEWGSSHAAVPRELSPLDL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 378.5; DB 24; LL. Pred. No. 6.7e-24; Indels 83;
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US-10-036-657-32

Sequence 32, Application US/10036657

GENERAL INFORMATION:

APPLICANT: Earl Francis Albone, et al.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES;

FILE REFERENCE: GF-0778B-C1

CURRENT APPLICATION UNMER: US/10/036,657

CURRENT FILING DATE: 2001-12-21

NUMBER OF SEQ ID NOS: 107

SEQ ID NO 32

LENGTH: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 47.28
Matches 84; Conservative
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US-10-036-657-32
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Best Local Similarity
Matches 82; Conserv
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US-60-200-109-981
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SEQ ID NO 981
LENGTH: 94
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Sequence 4967, Application US/60196718
GENERAL INFORMATION:
APPLICANT: BONAZZI, Vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOQ456
CURRENT APPLICATION NUMBER: US/60/196,718
CURRENT APPLICATION NUMBER: US/60/196,718
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:
APPLICANT. BOAZAL, Vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL00046
CURRENT APPLICATION NUMBER: US/60/192,739
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 4532
SEQ ID NO 3324
LENGTH: 92
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TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPPAPPAPALGKTGHLCSTGLDQCALGK 120
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                                                                                                      121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPR-ELSP 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 64;
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Pred. No. 2.1e-18;
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; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-192-739-3324
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Sequence 1, Application US/10016969
(SENERAL INFORMATION:
APPLICANT: Amylin Pharmaceuticals, Inc.
APPLICANT: Pittner, Richard
APPLICANT: Pottner, Richard
APPLICANT: Pottner, Richard
APPLICANT: Paternii, James
ITILE OF INVENTION: Deptide YY and Peptide YY Agonists for the Treatment of Metabolic
ITILE OF INVENTION: Disorders
ITILE OF INVENTION: US/10/016,969
CURRENT APPLICATION NUMBER: US/00-12-14
PRIOR APPLICATION NUMBER: US 60/256,216
PRIOR FILING DATE: 2000-12-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1.
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GENERAL INCUCHAGNICAL CONJUCHAGNICAL TO APPLICANT: Exidon, Dominique
APPLICANT: Exidon, Dominique
APPLICANT: Bridon, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudeau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PROFECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES
TITLE OF INVENTION: COMPONENTS
FILE REFERENCE: 2110
CURRENT FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR PELING DATE: 1999-09-10
PRIOR PELING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SEQ ID NOS: 1617
SEQ ID NOS: 1617
FENOMEN OF SEQ ID NOS: 1617
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19.3%; Score 186; DB 1; Length 36; 100.0%; Pred. No. 4e-08;
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                      100.0%; Prec. ...
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                                                                                                           30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR
                                                                                                                                                                                                                                                                                            ; Sequence 391, Application US/09657276; GENERAL INFORMATION:
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                                                       Conservative
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US-10-016-969-1
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Best Local Similarity
Matches 35; Conserva
        Query Match
Best Local Similarity
Matches 35; Conserv
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US-10-016-969-1
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TYPE: PRT
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APPLICANT: Bulter, Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Screen for Agents
TITLE OF INVENTION: Modify Feeding Behavior
FILE REFERENCE: 0899-63986
CURRENT APPLICATION NUMBER: FOT/US02/30533
PRIOR APPLICATION NUMBER: 60/324,406
PRIOR APPLICATION NUMBER: 60/324,406
PRIOR APPLICATION NUMBER: 60/3392,109
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 352
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                            APPLICANT: Bonazzi, vivien
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: MUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: C.0000417
CURRENT APPLICATION NUMBER: US/60/194,243
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 3242
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2397
LENGTH: 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 VPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPL 176
                                                                                        122 VPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPRELSPL 176
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                                                                                                                            ---PMYGERDKEDTLAFSEWGLPMLLPPGEFDSL 92
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Best Local Similarity 40.6%; Pred. No. 3.5e-18;
Matches 71; Conservative 5; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: VARIANT
COTATION: (1)...(92)
COTHER INFORMATION: Xaa = Any Amino Acid
US-60-194-243-2397
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Sequence 25, Application PC/TUS0230533
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                         Sequence 2397, Application US/60194243
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 K-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: HUMAN
                                                                                                                                                                                                                            RESULT 12
US-60-194-243-2397
                                            61 K----
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30 APLEPVYPGDNATPEOMAQYAADLRRYINMLTRPR 64 QQ ò

Search completed: March 1, 2003, 09:16:27 Job time : 145 secs

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March 1, 2003, 09:12:05 ; Search time 25 Seconds
(without alignments)
663.560 Million cell updates/sec
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964
1 MAAARLCLSLLLLSTCVALL......FSEWGSPHAAVPRELSPLDL 178
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pending Patents AA New:*

1: /cgn2 6/ptodata/2/paa/PCT NEW COMB.pep:*
2: /cgn2 6/ptodata/2/paa/US06.NEW COMB.pep:*
3: /cgn2 6/ptodata/2/paa/US06.NEW COMB.pep:*
4: /cgn2 6/ptodata/2/paa/US09.NEW COMB.pep:*
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7: /cgn2 6/ptodata/2/paa/US09.NEW COMB.pep:*
7: /cgn2 6/ptodata/2/paa/US00_NEW COMB.pe

Database :

	Description	Segmence 2	-25 Seguence 25.	Sequence 28	-28 Seguence 28.	-26 Seguence 26.	7 Sequence 27,	-26 Sequence 2	7 Sequence 27	Sequence 29	29	Sequence 32	2 Seguence 32	Seguence 3.		31	1 Sequence 31	0 Sequence 30	0 Sequence 30	Sequence 35	Seguence 35	Sequence 87	0 Seguence 71	11 Seguence 11	Semience 11	Seguence 71	
SUMMARIES	ID	PCT-US02-319	PCT-US02-305	PCT-US02-31944A	JS02-	PCT-US02-31944A	PCT-US02-31944A	PCT-US02-305	PCT-US02-305				PCT-US02-305	PCT-US02-31944A	PCT-US02-305	PCT-US02-319	PCT-US02-305	PCT-US02-319	PCT-US02-30533A-3	PCT-US02-31944A	PCT-US02-30533A-3		US-10-072-012-71	PCT-US02-31944A-	PCT-US02-30533A-1	US-10-072-01	
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de	Query Match Length	19.3	19.3	18.9	18.9	18.4	18.4	18.4	18.4	18.3	18.3	17.6	17.6	17.4	17,4	16.0	16.0	14.4	14.4	12.8	12.8	12.7	12.0	11.7		11.3	
	Score	186	186	182	182	177	177	177	177	176		169.5	9	168	168	154	154	139	139	123	123	122	116	113	113	109	,
	Result No.	П	7	m	4	S	φ	7	89	0	10	11	12	13	14	15	16	17	18	19	20	21	22			25	

Sequence 25, Application PC/TUS0230533A
GENERAL INFORMATION:
APPLICANT: Conley, Michael
APPLICANT: Low, Malcolm
APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Be

RESULT 2 PCT-US02-30533A-25

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Sequence 709, App	Sequence 711, App	Seguence 34, Appl	34.	1630	•	1675	631,	107,	107,	444	14	69	14,	69	14.	69	14.	Sequence 69, Appl
US-10-072-012-709	US-10-072-012-711	PCT-US02-31944A-34	PCT-US02-30533A-34	PCT-US02-40891-1630	PCT-US02-40892-617	PCT-US02-40891-1675	PCT-US02-40892-631	PCT-US02-28859-107	US-10-241-220-107	US-10-225-567A-444	US-10-150-811-14	US-10-150-811-69	US-10-131-409-14	US-10-131-409-69	US-10-139-854-14	US-10-139-854-69	US-10-150-813-14	US-10-150-813-69
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97	97	36	36	645	645	677	677	3014	3014	3014	3028	3028	3028	3028	3028	3028	3028	3028
11.3	11.3	11.0	11.0	10.8	10.8	10.8	10.8	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6	10.6
109	109	106	106	104.5	104.5	104	104	102	102	102	102	102	102	102	102	102	102	102
27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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TITLE OF INVENTION: Modification of Feeding Behavior
TITLE OF INVENTION: Modification of Feeding Behavior
FILE REPERENCE: 899-6372
CURRENT APPLICATION NUMBER: DCT/US02/31944A
CURRENT FILING DATE: 2002-09-24
PRIOR PRIOR APPLICATION NUMBER: US 60/324,406
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 335
SOFTWARE: PATENTIN Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
19.3%; Score 186; DB 1; 1
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 35; Conservative 0; Mismatches 0;
                                                               APPLICANT: Imperial College Innovations Limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
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                  ; Sequence 25, Application PC/TUS0231944A; GENERAL INFORMATION:
                                                                                  Bloom, Stephen R. Small, Caroline J. Batterham, Rachel L. Ghatei, Mohammad A. Cowley, Michael
                                                                                                                                                                                                   Cone, Roger
Low, Malcolm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Ovis aries PCT-US02-31944A-25
PCT-US02-31944A-25
                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 36
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APPLICANT:
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APPLICANT: Low, Malcolm
APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Modification of Feeding Behavior:
FILE REFERENCE: 899-63727
CURRENT APPLICATION UNMER: DCT/USO2/31944A
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 60/324,406
PRIOR APPLICATION NUMBER: US 60/324,406
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR APPLICATION NUMBER: US 60/392,109
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/392,109
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 335
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                        Score 182; DB 1;
Pred. No. 7.5e-07;
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GENERAL INFORMATION:
APPLICANT: Imperial College Innovations Limited
APPLICANT: Shall, Caroline J.
APPLICANT: Batterham, Rachel L.
APPLICANT: Ghatei, Mohammad A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Imperial College Innovations Limited
         CURRENT APPLICATION NUMBER: PCT/USO2/30533A
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 60/324,406
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2007-06-28
NUMBER OF SEQ ID NOS: 352
SOFTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 36
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Best Local Similarity 97.1%;
Matches 34; Conservative
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Matches 33; Conservative
FILE REFERENCE: 899-63986
                                                                                                                                                                                                                                                                                  ; ORGANISM: Felis catus
PCT-US02-30533A-28
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PCT-US02-31944A-27
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: Cone, Roger
APPLICANT: Low, Malcolm
APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding
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APPLICANT: Imperations Stephen R.
APPLICANT: Balom, Stephen R.
APPLICANT: Batterham, Rachel L.
APPLICANT: Gate; Mohammad A.
APPLICANT: Cowley, Michael
APPLICANT: Cowley, Michael
APPLICANT: Cowley, Michael
APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Modification of Feeding Behavior
FILE REFERENCE: 899-637-8
CURRENT APPLICATION NUMBER: PCT/US02/31944A
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Best Local Similarity 97.1%; Pred. No. 7.5e-07;
Matches 34; Conservative 1; Mismatches 0
  FILE REFERENCE: 899-63986
CURRENT APPLICATION NUMBER: PCT/USO2/30533A
CURRENT FILING DATE: 2002-09-24
FILING APPLICATION NUMBER: US 60/324,406
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 352
SOFTWARE: PatentIn version 3.1
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19.3%; Score 186; DB
Best Local Similarity 100.0%; Pred. No. 3.8
Matches 35; Conservative 0; Mismatches
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PRIOR PEPLICATION INVIBER: US 60/324,406
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/392,109
PRIOR FILING DATE: 2002-01-20
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SOFTWARE: Patentin version 3.1
SEQ ID NO 28
LENGTH: 36
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; ORGANISM: Felis catus
PCT-US02-31944A-28
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ORGANISM: Ovis aries
PCT-US02-30533A-25
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LENGTH: 36
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Sequence 29, Application PC/TUS0230533A
GENERAL INFORMATION:
APPLICANT: Cowley, Michael
APPLICANT: Cowley, Malcolm
APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Be
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Pred. No. 1.8e-06;
2; Mismatches 0; Indels
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Pred. No. 2.1e-06;
1; Mismatches 1; Indels
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FORMATION:

(T: Imperial Colley.
ANT: Ball Caroline J.
LICANT: Small, Caroline J.
LICANT: Batterham, Rachel L.
PLICANT: Cowley, Michael
APPLICANT: Cone, Roger
APPLICANT: Cone, Maclael
APPLICANT: Cone, Maclae
APPLICANT: Cone, Canada
APPLICANT: Cone, Cone, Canada
APPLICANT: Cone, Cone, Canada
APPLICANT: Cone, Cone, Canada
APPLICANT: Cone, Canada
APPLICANT: Cone, Canada
APPLICANT: Cone, Canada
APPLICANT: Cone, Cone, Cana
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                             CURRENT APPLICATION NUMBER: PCT/USO2/30533
CURRENT FLILIG DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 60/324,406
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 352
SOFTWARE: PATENT Version 3.1
LENGTH: 36
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ilarity 94.3%;
Conservative
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; ORGANISM: Canis familiaris
PCT-US02-30533A-27
   FILE REFERENCE: 899-63986
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Best Local Similarity
Matches 33; Conserv
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Sequence 27, Application PC/TUS0230533A
GENERAL INFORMATION:
APPLICANT: Cowley, Michael
APPLICANT: Come, Roger
APPLICANT: Low, Malcolm
APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Be
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APPLICANT: Low, Malcolm
APPLICANT: Low, Malcolm
APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Be
FILE REFERENCE: 899-63986
CURRENT APPLICATION NUMBER: PCT/US02/30533A
CURRENT APPLICATION NUMBER: US 60/324,406
PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: US 60/322,109
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 352
SOFTWARE: Patentin version 3.1
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18.4%; Score 177; DB 1; Length 36;
Best Local Similarity 94.3%; Pred. No. 1.8e-06;
Matches 33; Conservative 2; Mismatches 0; Indels
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   APPLICANT: Cone, NCSC.
APPLICANT: Low, Malcolm
APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TILEOP INVENTION: Modification of Feeding Behavior
FILE REFERENCE: 899-63727
CURRENT APPLICATION NUMBER: PCT/USO2/31944A
CURRENT FILING DATE: 2002-09-24 406
PRIOR APPLICATION NUMBER: US 60/324,406
PRIOR APPLICATION NUMBER: US 60/324,106
PRIOR PLING DATE: 2001-09-24
PRIOR PLING DATE: 2002-01-10
PRIOR PLING DATE: 2002-01-10
PRIOR FLING DATE: 2002-06-28
NUMBER FO FEG ID NOS: 335
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 27
LENGTH: 36
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GENERAL INFORMATION:
APPLICANT: Cowley, Michael
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Best Local Similarity
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ORGANISM: Sus sp.
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LENGTH: 36
APPLICANT:
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Matches
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APPLICANT: Comey, Michael
APPLICANT: Cone, Roger
APPLICANT: Low, Maloolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding B
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APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Modification of Feeding Behavior-
FILE REFERENCE: 899-63727
                                                                                                                                                                                                                                                                                                                                  Score 169.5; DB 1
Pred. No. 6.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Imperial College Innovations Limited
         CURRENT APPLICATION NUMBER: PCT/US02/30533A;
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 60/324,406
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/392,109
PRIOR PRILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 352
SOFTWARE: Patentin version 3.1
SQU ID NO 32
LENGTH: 37
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PRIOR FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: GB 0200507.2
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 335
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application PC/TUS0231944A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                     17.6%;
91.7%;
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.77
Matches 33; Conservative
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Matches 32; Conservative
                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Cavia porcellus
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                                                                                                                                                                                                                                                                                        PCT-US02-30533A-32
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PCT-US02-30533A-3
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APPLICANT:
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APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Assessment of Neurons in the Arcuate Nucleus to Modify Feeding Be
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APPLICANT: Low, Malcolm
APPLICANT: Butler, Andrew
TITLE OF INVENTION: Modification of Feeding Behavior
FILE REFERENCE: 899-63727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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Pred. No. 2.1e-06;
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17.6%; Score 169.5; DB 1
Best Local Similarity 91.7%; Pred. No. 6.3e-06;
Matches 33; Conservative 2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Imperial College Innovations Limited
         CURRENT APPLICATION NUMBER: PCT/US02/30533A
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 60/324,406
PRIOR FILING DATE: 2001-09-24
PRIOR PILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 352
SOFTWARE: Patentin version 3.1
SEQ ID NO 29
LENGTH: 36
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CURRENT FILING DATE: 2002-09-24
PRIOR PAPLICATION NUMBER: 95 60/324,406
PRIOR PILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR PLING DATE: 2002-01-10
PRIOR PAPLICATION NUMBER: US 60/392,109
PRIOR FILING DATE: 2002-01-10
PRIOR PRIOR PILING DATE: 2002-01-10
PRIOR PRIOR PILING DATE: 2002-01-10
SRIGHT SPICE SEQ ID NOS: 335
SOFTWARE: PARENTIN VETSION 3.1
SEQ ID NO 32
LENGTH: 37
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APPLICANT: Cowley, Michael
APPLICANT: Cone, Roger
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Small, Caroline J.
Batterham, Rachel L.
Ghatei, Mohammad A.
Cowley, Michael
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Best Local Similarity 94.3%;
Matches 33; Conservative
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FILE REFERENCE: 899-63986
                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Bos taurus
PCT-US02-30533A-29
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PCT-US02-30533A-32
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17.4%; Score 168; DB 1; Length 36;
Best Local Similarity 91.4%; Pred. No. 8e-06;
Matches 32; Conservative 1; Mismatches 2; Indels
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16.0%; Score 154; DB 1; Length 36;
Best Local Similarity 82.9%; Pred. No. 8.4e-05;
Matches 29; Conservative 1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Imperial College innovations inmitted
APPLICANT: Batterham, Stephen R.
APPLICANT: Batterham, Rachel L.
APPLICANT: Ghatei, Mohammad A.
APPLICANT: Ghatei, Mohammad A.
APPLICANT: Ghatei, Mohammad A.
APPLICANT: Cone, Roger
APPLICANT: Cone, Roger
APPLICANT: Low, Malchael
APPLICANT: Bow, Malcon
TITLE OF INVENTION: Modification of Feeding Behavior
FILE REFERENCE: 899-6372.
CURRENT APPLICATION NUMBER: PCT/USO2/31944A
CURRENT FILING DATE: 2002-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2001-09-24
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-01-10
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 335
SOFTWARE PATENTIN VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 31, Application PC/TUS0231944A
GENERAL INFORMATION:
APPLICANT: Imperial College Innovations Limited
APPLICANT: Small, Caroline J.
APPLICANT: Small, Caroline J.
APPLICANT: Ghatei, Mohammad A.
APPLICANT: Cowley, Michael
FILE REFERENCE: 899-63986

CURRENT APPLICATION NUMBER: PCT/US02/30533A

CURRENT FILING DATE: 2002-09-24

PRIOR APPLICATION NUMBER: US 60/324,406

PRIOR FILING DATE: 2001-09-24

PRIOR PILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 352

SOFTWARE: PALENT NOS: 352

SOFTWARE: PALENT NOS: 352

SEQ ID NO 3

LENGTH: 36
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; ORGANISM: Mus musculus
PCT-US02-31944A-31
                                                                                                                                                                                                                                                                                          TYPE: PRT
GORGANISM: Homo sapiens
PCT-US02-30533A-3
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LENGTH: 36
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Sequence 31, Appl Sequence 10, Appl Sequence 5, Appli Sequence 1, Appli Sequence 32, Appli

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Sequence 18, A Sequence 120,

Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence Sequence Sequence

Sequence 3, Sequence 1, Sequence 1, Sequence 4, Sequence 2, Sequence 5, Sequence 5, Sequence 5,

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METHODS OF TREATING NON-INSULIN DEPENDENT DIABETES MELLITUS WITH PANCREATIC POLYPEPTIDE
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19.3%; Score 186; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.7e-12;
Matches 35; Conservative 0; Mismatches 0; Indels
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US-08-338-395-3

US-08-328-151-24

US-08-907-403A-1

US-09-181-941.3

PCT-US95-14303-3

US-08-264-030-1

US-08-264-030-1

US-08-338-395-4

US-08-111-941-5

PCT-US95-14303-4

US-09-111-941-5

PCT-US95-14303-4

US-08-397-633A-31

US-08-397-633A-31

US-09-150-460B-10

US-09-150-461-5

US-09-150-461-5

US-09-150-461-15

US-09-150-461-15

US-09-150-461-15

US-09-347-991-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TAYLOR, IAN L.
APPLICANT: GETTYS, THOMAS
TITLE OF INVENTION: METHODS OF TREATING NON
TITLE OF INVENTION: DEPENDENT DIABETES MELL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: RESEDLE & ROSENBERG, P.C.
STREET: Suite 1200, 127 Peachtree Street
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Patent No. 5830434
GENERAL INFORMATION:
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   CITY: Atlanta
STATE: Georgia
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   168.945 Million cell updates/sec
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1 MAAARLCLSILILLSTCVALL......FSEWGSPHAAVPRELSPLDL 178
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Sequence 2,
Sequence 2,
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Sequence 12
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(Sgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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(Sgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(Sgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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US-09-054-333-1
US-09-924-906-1
US-09-229-906-1
US-09-221-994-6
US-08-221-750A-5
US-08-338-395-2
US-08-329-151-2
US-08-329-151-2
US-08-329-151-2
US-09-047-986B-1
US-09-047-986B-1
US-09-047-986B-1
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US-08-555-669-12
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Perfect score:
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APPLICANT: Mutter, Manfred
APPLICANT: Lacroix, Jean S.
APPLICANT: Lacroix, Jean S.
APPLICANT: Targinann, Eric
TITLE OF INVENTION: Template Associated NPY Y2-Receptor
TITLE OF INVENTION: Agonists
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Vinson & Elkins LLP
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                              OPERATING SYSTEM: FC-DUS/MS-LUOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/994,946A
FILING DATE: 19-DEC-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Inhen, Jeffrey L., REGISCHATION NUMBER: 28,957
REFRENCE/DOCKET NUMBER: 23.28-110
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 6:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.
ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 10.7%; Score 103.5; DB 3; Best Local Similarity 39.1%; Pred. No. 0.0025; Matches 25; Conservative 12; Mismatches 18;
ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C. STREET: 555 13th Street NW, Suite 701-E CITY: Washington
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/09229900
; Patent No. 6288029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-994-946A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                   20004
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US-09-229-900-1
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Patent No. 6046317
GENERAL INFORMATION:
APPLICANT: Karvonen, Matti
APPLICANT: Resonen, Ullamari
APPLICANT: Pesonen, Ullamari
APPLICANT: Pusitupa, Matti
APPLICANT: Pusitupa, Matti
APPLICANT: Presonen, Ullamari
APPLICANT: Presonen, Ullamari
APPLICANT: Thorage of Invention: A DNA Molecule Encoding a Mutant
TITLE OF INVENTION: Thereof
NUMBER &P SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
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Sequence 1, Application US/09054393
Sequence 1, Application US/09054393
GENERAL INFORMATION:
APPLICANT: Mutter, Manfred
APPLICANT: Lacroix, Jean S.
APPLICANT: Grouxmann, Eric
TITLE OF INVENTION: Template Associated NPY Y2-Receptor
TITLE OF INVENTION: Agonists
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vinson & Elkins LLP
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
10.7%; Score 103.5; DB 3; Length 97;
Best Local Similarity 39.1%; Pred. No. 0.0025;
Matches 25; Conservative 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COMPRY: U.S.
ZIP: 20004-1008
ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BMR350/48000
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 639-6684
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: not relevant
MOLECULE TYPE: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: N
ANTI-SENSE: NO
US-09-054-393-1
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                                    RESULT 2
US-09-054-393-1
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SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/221,750A FILING DATE: 31-MAR-1994 CLASSIFICATION: 435
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Fatent No. 5328899
GENERAL INFORMATION:
APPLICANT: Bublik, Jaroslav H.
APPLICANT: Brown, Marvin R.
APPLICANT: Scott, Neal A.
TITLE OF INVENTION: NPY PEPTIDE ANALOGS
NUMBER OF SEQUENCES: 14
CORRESPONDENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fitch, Even, Tabin & Flannery
STREET: 4250 Executive Square, Suite 510
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Mismatches
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,619
FILING DATE: 15-MAR-1993
ATTORNEY/AGBNT INFORMATION:
NAME: Carroll, Alice O.
REGISTRATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: ACC93-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 505 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55; Conservative
                   NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                     ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
   FITLE OF INVENTION:
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Best Local Similarity
Matches 55; Conserv
                                                                                                 Lexington
                                                                                                                                     USA
                                                                                               CITY: Les
STATE: M
COUNTRY:
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                                                                             STREET:
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Patent No. 6312898
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: Korvonen, Matti
APPLICANT: Besonen, Ullamari
APPLICANT: Desciupa, Matti
TITLE OF INVENTION: Diagnosis of a Person's Risk of Developing
TITLE OF INVENTION: Atherselerosis or Diabetic Retinopathy Based on Leucine
TITLE OF INVENTION: 7 to Proline 7 Polymorphism in the Prepro-Neuropeptide
TITLE OF INVENTION: 7 Gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                              1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                                                                                                                                                                                                                                                                                                                      1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
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                                                                                                                                                                                                                                                                                     Score 103.5; DB 4; Length 97; ;Pred. No. 0.0025; .2; Mismatches 18; Indels
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; Pred. No. 0.0025;
12; Mismatches 18; Indels
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Patent No. 5643747
CENERAL INFORMATION:
APPLICANT: Baker, Steven M.
APPLICANT: Deich, Robert A.
TITLE OF INVENTION: Genes for the Export of Pertussis
                                                                                                                                                                                                                                                                                                                          12; Mismatches
REFERENCE/DOCKET NUMBER: BMR350/48000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 2328-112.A
CURRENT APPLICATION NUMBER: US/09/291,994
CURRENT FILING DATE: 1999-04-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VEY: 2.0
                 TELECOMMUNICATION INFORMATION: TELEPHONE: (202)639-6585
                                                                                                             LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
                                                 TELEFAX: (202)639-6604
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.7%;
39.1%;
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Best Local Similarity 39.1%
                                                                                                                                                                                                                                                                                   Query Match 10.73
Best Local Similarity 39.13
Matches 25; Conservative
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                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                               ANTI-SENSE: NO
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US-09-291-994-6
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58 NMLTRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPAPAPALGKTGHLCSTGLDQCA 117
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E: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
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11;

Gaps

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Query Match
10.3%; Score 99; DB 1; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels
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10.3%; Score 99; DB 1; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: McFadden, David W
APPLICANT: McFadden, David W
TITLE OF INVENTION: TREATMENT OF PANCREATIC TUMORS WITH
TITLE OF INVENTION: PEPTIDE YY AND ANALOGS THEREOF
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: POMS, SMITH, LANDE & ROSE
STREET: 2029 Century Park East 38th Floor
CITY: Los Angeles
STREET: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: USAC

ZIP: 90657

COMPUTER READABLE FORM:

MEDIUM TYBE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/338,395

FILING DATE:

CLASSIFICATION: 514

ATTORNEY AGENT INFORMATION:

NAME: Oldenkamp, David J

REGISTRATION NUMBER: 107012

REFERENCE/DOCKET NUMBER: 107012

TELECHMUNICATION INFORMATION:

TELEPHONE: 310-788-5046

TELEPHONE: 310-788-5046

TELEPHONE: 310-738-5046

TELEPHONE: 310-738-5046

TELEPHONE: 310-738-5046
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                                                                                                                                                                                                                                                                                                                                                                                                    31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR
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US-08-329-151-1
; Sequence 1, Application US/08329151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08338395
Patent No. 5574010
                                                                                                                                                                                                  ORGANISM: porcine peptide YY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide ORIGINAL SOURCE: ORGANISM: HUMAN PEPTIDE YY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 36 amino acids
TYPE: amino acid
TOPOLOGY: linear
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                          MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                          LENGTH:
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Patent No. 5574010
GENERAL INFORMATION:
APPLICANT: McFadden, David W
TITLE OF INVENTION: PEPTIDE YY AND ANALOGS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                      COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM:
PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/882,923
FILING DATE: 19920512
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/503,198
FILING DATE: 30-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/219,596
FILING DATE: 15-JUL-1988
ATTORNEY/AGENT INFORMATION:
NAMME: SCHUMMIN, James J.
NEGISTRATION NUMBER: 52864
TELECOMMUNICATION INFORMATION:
TELEPRACE (19-552-1311
TELERACE (19-552-1311
TELEPRACE (19-552-1311
TELERACE (19-552-1311
TELERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.3%; Score 99; DB 1; Best Local Similarity 47.1%; Pred. No. 0.002; Matches 16; Conservative 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 36 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide US-07-882-923-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-338-395-1
           COUNTRY:
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| GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Muter, Manfred APPLICANT: Lacroix, Jean S. APPLICANT: Groumman, Eric TITLE OF INVENTION: Agonists NUMBER OF SEQUENCES: 8 |
| NUMBER OF SEQUENCES: 8 |
| CORRESPONDENCE ADDRESSE: ADDRESSEE: Vinson & Elkins LLP STREET: 1455 Pennsylvania Avenue, N.W. CITY: Machington 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
10.3%; Score 99; DB 1; Length 36;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,393
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGRAT INFORMATION:
NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
REGISTRATION NUMBER: 36,912
REFERENCE/DOCKET NUMBER: BMR350/48000
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
                       APPLICATION NUMBER: US/08/329,151
CLASSIFICATION NUMBER: US/08/329,151
FILING DATE: US/08/329,151
FILING DATE: 3/29/33
APPLICATION NUMBER: 08/038,534
FILING DATE: 3/29/33
APPLICATION NUMBER: 08/19/33
ATTONER/ASDRY INFORMATION:
REGISTRATION NUMBER: 30,162
REGISTRATION NUMBER: 0.0537/105001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE: (617) 542-5070
TELEFRANCE: (617) 542-8906
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STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202)639-6604
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.
ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 36
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-329-151-2
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US-08-329-151-2
i Sequence 2, Application US/08329151
i Patent No. 5604203
i GENERAL INFORMATION:
APPLICANT: Balasubramaniam, A.
i TITLE OF INVENTION: THEREOF
i TITLE OF INVENTION: THEREOF
i NUMBER OF SEQUENCES: 30
i CORRESPONDENCE'ADDRESS:
i ADDRESSEE: Fish & Richardson
STREET: 225_Franklin Street
                       GENERAL INFORMATION:
APPLICANT: Balasubramaniam, A.
APPLICANT: Balasubramaniam, A.
TITLE OF INVENTION: ANALOGS OF PEPTIDE YY AND USES.
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
10.3%; Score 99; DB 1;
Best Local Similarity 47.1%; Pred. No. 0.002;
Matches 16; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION NUMBER: US/08/329,151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514 CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/038,534
APPLICATION NUMBER: 08/109,326
FILING DATE: 08/19/93
ATTONREY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTURNB 1 AND ATTURN A
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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GENERAL INFORMATION:

APPLICANT: Manfred
APPLICANT: Lacroix, Jean S.
APPLICANT: Grouzmann, Eric
TITLE OF INVENTION: Template Associated NPY Y2-Receptor
TITLE OF INVENTION: Agonists
NUMBER OF SEQUENCES:
ADDRESSEE: Vinson & Elkins LLP
STREET: 1455 Pennsylvania Avenue, N.W.
CITY: Washington
STREET: D.C.
COUTRY: U.S.
ZIP: 20004-1008
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.3%; Score 99; DB 3; Length 36; 47.1%; Pred. No. 0.002; tive 11; Mismatches 7; Indels
                                                                                                                                         COUNTRY: USA

ZIP: 45202-4182

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,900
ADDRESSEE: Frost & Jacobs, L.L.P.
STREET: 2500 PNC Center, 201 East Fifth St.
CITY: Cincinnati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PIKPEAPGEDASPEELNRYYASLRHYLNLVTRQR 35
                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Word 97
CURRENT APPLICATION DATA:
PELLING DATE: 25 March 1998
FILING DATE: 25 March 1998
CLASSIFICATION: 514
ATTORNEY AGENT INFORMATION:
NAME: Krietyne A. Bullock
REGISTRATION NUMBER: 42,371
REFERENCE/DOCKET NUMBER: 9183030/508
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1851-673
TELEFEX: (513) 651-691
TELEFEX: (513) 651-691
TELEFEX: (513) 651-673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)639-6585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/09229900
; Patent No. 6288029
; GENERAL INFORMATION:
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NAME: Sanzo, Michael A.
REGISTRATION NUMBER: 36,912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 47.1%
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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CLASSIFICATION:
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US-09-229-900-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: CHICLINIALI
STATE: CHICLINIALI
STATE: OHOUREX: USA
ZIP: 45202-412
COMPUTER READALE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/09/047,986B
FILING DATE: 25 MARCH 1998
CLASSIFICATION: 514
ATTORINY AGENT INFORMATION:
NAME: KISTYNE A. Bullock
REGISTRATION NUMBER: 42,371
REFERENCE/DOCKET NUMBER: 9183030/508
TELECOMMUNICATION HYDERAMION:
TELEPHONE: (513) 651-6731
TELEPKX: (513) 651-6981
TELEFXX: 21-4396 F&J CI.
SEQUENCE CHARACTERISTICS:
LENNORM TONE SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09047986B
; Patent No. 6046167
; GENERAL INFORMATION:
   APPLICANT: Balasubramanian, Ambikaipakan
   TITLE OF INVENTION: PEPTIDE YY ANALOGS
; CORRESPONDRACE ADDRESS: 20
; ADDRESSEE: ADDRESSE: ADDRESSEE: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 10.3%; Score 99; DB Best Local Similarity 47.1%; Pred. No. 0.00 Matches 16; Conservative 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                           2 PIKPEAPGEDASPEELNRYYASLRHYLNLVTRQR 35
                                                                                                                                                                                                                                                                                                                                                                  31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09047986B
Patent No. 6646167
GENERAL INFORMATION:
APPLICANT: Balasubramanian, Ambikaipakan
TITLE AP INFORMION: PEFFIDE YY ANALOGS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 amino acids
   not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-047-986B-1
                                     MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-047-986B-1
                                                                                                                   ; ANTI-SENSE:
US-09-054-393-2
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0; Gaps
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                                                                                                                                                                                                                                                                       TELEFAX: (202)639-6604

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-09-229-900-2
                                                                                                                                                                                                                                                                            ò
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Search completed: March 1, 2003, 09:13:57 Job time : 33 secs

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GenCore version 5.1.3

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein earch, using sw model

Run on:

March 1, 2003, 09:11:12; Search time 30 Seconds
(without alignments)
1222.546 Million cell updates/sec

Title:
Perfect score: 964
Sequence:
1 MAAARLCLSLLLSTCVALL......FSEWGSPHAAVPRELSPLDL 178
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues
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btal number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SPTREMBL_21:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	de			SUMMAKIES	
Score	Query Match	Query core Match Length DB ID	DB	ID	Description
١	17.5	59	9	O9GKL0	Q9gkl0 sus scrofa
	12.0				O919d3 ictalurus p
	11.8				Q91xd0 mus musculu
_	11.5	542	7	068872	O68872 myxococcus
'n	11.5				Q925v2 mus musculu
'n	11.5				Q90wf4 paralichthy
o	11.0				Q8spf7 ovis aries
'n	10.9				Q9xsw6 macaca mula
ın	10.9				Q90wf3 paralichthy
'n	10.8				Q9tsi6 ovis aries
4	10.8				Q9pw68 typhlonecte
102.5	10.6				O52861 bacillus su
a	10.6				Q9rkr9 streptomyce
a	10.6				Q9nyq6 homo sapien
_	10.5				Q9dgk7 cyprinus ca
'n	10.1				032062 bacillus su

neem beembee e	090wiz paralichthy 091ym9 mus musculu 09dbd5 mus musculu 09axnl botryocladi 040955 rubella vir 09n3y8 caenorhabdi 09stpl arabidopsis 020927 caenorhabdi
20 09J6K9 20 09J6K9 20 09J0K93 20 09J0K93 20 09J1E5 20 09J0E3	13 Q90WF2 11 Q91YM9 11 Q9DBD5 12 Q40955 5 Q9N3Y8 10 Q9STP1 5 Q20927
2129 2115 2115 36 1203 4 1203 2116 2116 1790 1790 1790 1790 1790 1790 1790 1790	97 675 1123 1712 2116 2344 577 295
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	92.5 92.5 92.5 92.5 91.5 91.5
11112222222222222222222222222222222222	8 6 6 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6

ALIGNMENTS

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96 APSRPALGKTGHLCSTGLDQCALGKMVPTGRYETGGLAPGHSACPCCLFPPRYGKRKED 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 YPGDNATPEQMAQYAADLRRYINMLTRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P. SEQUENCE FROM N.A.

Han X.G., Tuch B.E.;

Han X.G., Tuch B.E.;

"Partial porcine paneeatic polypeptide cDNA sequence (3'end).";

"Partial porcine paneeatic polypeptide cDNA sequence (3'end).";

"Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

"I. Submitted (19-2) to the EMBL/DDBJ databases.

"I. Submitted (19-2) to the EMBL/GenBank/DDBJ databases.

"I. Submitted (19-2) to the EMBL/DDBJ databases.

"I. Submitted (19-2) to the EMBL/DDB
                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 17.5%; Score 169; DB 6; Length 59; 1 Similarity 31.2%; Pred. No. 2.6e-08; 44; Conservative 5; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 1 1 SEQUENCE 59 AA; 6683 MW; 9A199783B9E29FCD CRC64;
                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
NCBI_TaxID=9823,
                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
1-WAR-2002 (TrEMBLrel. 20, Last annotation update)
Panceatic polypeptide (Fragment).
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 AA.
                                                                       PRT;
                                                                           PRELIMINARY;
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                                       Q9GKL0
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SC OCC BETT BY

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77 -----GTLGPLH-----IPGHTLSPAPAP-----APSRPALGKTGHLCST-GLDQC 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 SRHARRNPAGPSRRCGPPRKSTPTRCCTPCPAPPRCRARPSAPA-PSAGRTCPTAGPSSC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASG-CCPTGRC---GSAPGPTPHGAEPSPPSQSPSPAPASSGGRRRTHPRPARASAAGAT 207
                                                                                                                                                                                                 10 LLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINMLTRPRCVPQL 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GAQGAPLEPV-YPGDNATPEQMAQYA----ADLRRY---INMLTRPRCVPQLGREIPAP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GARPPPTETASYPPPQAVPGPCAPRAPPRSPPRRRHRGSRHRSFRPTCARRSGRRCPAP 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harris B.Z., Singer M.; "Identification of the Myxococcus xanthus argE
                                                                                                                                                                                                                          ||:| |::|| | |::|| |----DAYPAKPEAPGEDASPEELSRYYASLRHYLNLVTRQR----Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                            DB 11; Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.5%; Score 111; DB 2; Length 542; Best Local Similarity 28.6%; Pred. No. 0.053; Matches 54; Conservative 5; Mismatches 58; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria, Proteobacteria, delta subdivision, Myxobacteria, Myxococcales, Cystobacterineae, Myxococcaceae, Myxococcus.
                                                                                                       / Match 11.8%; Score 113.5; DB 11; Length Local Similarity 37.3%; Pred. No. 0.0047; nes 25; Conservative 16; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Bacteriol. 180:6412-6414(1998).
EMBL, APOS5904; AAC82365.1; -.
Hypothetical protein.
SEQUENCE 542 AA; 57203 MW; DA7E39075A86A8BC CRC64;
                                                        7AF165A1052C3249 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 57.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
ProDom; PD001267; Pancreatic hormn; 1.
PROSITE; PS00265; PANCREATIC HORMONE 1; UNKNOWN 1.
PROSITE; PS50276; PANCREATIC HORMONE 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
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                                                                   11064 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myxococcus xanthus.
                                                                   98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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GKRDVPA 71
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                                                                   SEQUENCE
                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                    068872
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Matches
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Leonard J.B.K., Waldbieser G.C., Silverstein J.T.;

Leonard J.B.K., Waldbieser G.C., Silverstein J.T.;

Leonard J.B.K., Waldbieser G.C., Silverstein J.T.;

Louncrale Y (NPY) sequence and distribution in channel catfish

(Ictalurus punctatus).";

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.

R FMEL; AF267164; AAF71617.1; -..

R HSSP; P01303; IRON.

R RFam; PF00159; hormone3; 1.

R PRINTS; PR00159; hormone3; 1.

R PRINTS; PR00279; PANCHORMONE.

R PRODOM; P0001267; Pancreatic_hormn; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
    ----PRYGKRDEED 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARLCL---SLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Siluriformes,
Ictaluridae, Ictalurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ٠<u>.</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 12.0%; Score 115.5; DB 13; Length
Local Similarity 32.9%; Pred. No. 0.003;
les 26; Conservative 19; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC010821, AH110821.1; ...
InterPro; IFR001955; Pancreatic_hormn.
Pfam; PF00159; hormone3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 AA; 10729 MW; 9AE19EAFBE24C6B5 CRC64;
                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                           [ctalurus punctatus (Channel catfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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Mus musculus (Mouse).
                                          156 TLAFSEWGSPHAAVPRELSPL 176
                                                                                     38 LLDL-KCSSLHAAAPRELSPM 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TRPRCVPQLGREIPAPGTL 79
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                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7998;
                                                                                                                                                                                                                                                                                                      Neuropeptide Y
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Matches
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59

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12;

72; Gaps

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01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19, Neuropeptide Y.
                                                                                                                             Neuropeptide Y precursor.
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                      28
64
                                                                                                                                                        Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
es 26; Conserv
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68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TRPR 64
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                                                                                          01-JUN-2002
                                                                                                      01-JUN-2002
01-JUN-2002
      63
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                               08SPF7;
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       63
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                                                                                                                                                                                                                                                                                     1 MAAARLCLSILLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                                                                                                                                                                                                7; Gaps
                                                                                                                                                                                                                                                                                                    4 ARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINMLTRP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Taylor B.A., Wark C., Schroeder D., Phillips S.J.;

"Multiple obesity QTLs identified in an intercross between the NZO (New Zealand obese) and the SM (small) mouse strains.";

Mamm. Genome 12.95-103 (2001).

EMBL; AF286198; AAG01330.1;

EnterPro; IPR001955; Pancreatic_hormn.

Probom; PD00159; hormone3; 1.

PROSITE; PS00265; PANCREATIC_HORMONE_1; UNKNOWN_1.

PROSITE; PS00265; PANCREATIC_HORMONE_2; 1.
 Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neopterygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes; Pleuronectoidei, Paralichthyidae, Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organs during the larval stage of Japanese flounder, Paralichthys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neuropeptide Y related peptides in the digestive
                                                                                                                                                                                                                                     11.5%; Score 110.5; DB 11; Length 89; 42.2%; Pred. No. 0.0079; Live 11; Mismatches 19; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 110.5; DB 13; Lellyll.
39.3%; Pred. No. 0.0089;
.^ Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production PD00126; Pancreatic hormn; 1.
PROSITE; PS00265; PANCREATIC HORMONE 1; UNKNOWN 1.
PROSITE; PS50276; PANCREATIC HORMONE 2; 1.
SEQUENCE 99 AA; 11215 MW; 6FEED47F24CF6498 CRC64;
                                                                                                                                                                                                             89 AA; 9943 MW; AE6052615A59D96A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                99 AA.
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InterPro; IPR001955; Pancreatic_hormn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                            MEDLINE=21077529; PubMed=11210195;
                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paralichthys olivaceus (Flounder).
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01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00159; hormone3; 1
                                                                                                                                                                                                                                                               27; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kurokawa T., Suzuki T.;
"Development of neuroper
                                                                                                                                                                                                                                                  Local Similarity
                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=8255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 ALLCLSAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuropeptide Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                      TRPR 64
                                                                                                                                                                                                                                                                                                                                                                TROR 63
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                                                                                                                                                                                                            SEQUENCE
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Matches
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1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Abler L.A., Golos T.G., Terasawa E.;
"Developmental changes in NPY mRNA expression in female rhesus
                                                                                                                                                                                                                                                                                                                                                                                                            11.0%; Score 106; DB 6; Length 97; 40.6%; Pred. No. 0.022; Live 13; Mismatches 23; Indels
                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ILE DE FRANCE; TISSUE=HYPOTHALAMUS;
Pillon D., Bruneau G.;
"Nucleotide sequence of Ovine preproneuropeptide Y.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ417904; CAD10677.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
EMBL; AF162280; AAD43583.1; -.
HSSP; P01303; IRON.
                                                                                                                                                                                                                                                                                                                                                                           6C2209A361CF8583 CRC64;
                                              Last sequence update)
Last annotation update)
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Last annotation update)
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97 AA.
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Pfam; PF00159; hormone3; 1.
PRINTS; PR00278; PANCHORMONE.
PRODOM; PB0001267; Pancreatic_hormn; 1.
PROSITE; PS00265; PAH; 1.
PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
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                                Created)
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                                                                                                                                                                                                                                                                                                                                                                             10750 MW;
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PRELIMINARY;
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[1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                          61 TRPR 64
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NON_TER
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                      Gaps
                                                                         1 MAAARLCLSLILLISTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                        2 LGSKRLGLSGLTLALSLLVCLGAL--AEAYPSKPDNPGEDAPAEDMARYYSALRHYINLI 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropeptide Y (Eragment).

Ovis aries (Sheep).

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidea; Caprine; Oyis.
                                                                                                                                                                                                                                                                     Paralichthys olivaceus (Flounder).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,

Eukaryota, Neopterygii, Teleostei, Neoteleostei;

Acanthomorpha, Acanthopterygii, Percomorpha, Pleuronectiformes;

Pleuronectoidei, Paralichthyidae, Paralichthys.
                                                                                                                                                                                                                                                                                                                                                YEQUENCE FROM N.A.
TISSUB-BRAIN;
Kurokawa T., Suzuki T.;
"Development of neuropeptide Y related peptides in the digestive "Development of neuropeptide of Japanese flounder, Paralichthys
                                                      5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
10.9%; Score 105; DB 13; Length 99;
Best Local Similarity 34.4%; Pred. No. 0.028;
Matches 22; Conservative 14; Mismatches 26; Indels
                                Length 97;
                               10.9%; Score 105; DB 6; Length 97 40.6%; Pred. No. 0.027; cive 13; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB055212; BAB62410.1; -.
InterPro; IPR001955; Pancreatic_hormn.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00159; hormone3; 1.
ProDom; PD001267; Pancreatic hormn; 1.
PROSITE; PS00265; PANCREATIC HORMONE 1; UNKNOWN 1.
SEQUENCE 99 AA; 11179 MW; 32F6C21217CB1984 CRC64;
             10840 MW; 2D2209BAC20BD5EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                        Local Similarity
les 26; Conserv
             97 AA;
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   Amidation.
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               SEQUENCE
                                   Query Match
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                                                       Matches
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Q90WF3
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Peptides 22:325-334 (2001)

- FUNCTION: NPY IS IMPLICATED IN THE CONTROL OF FEEDING AND IN

SECRETION OF GONADOTROPHIN-RELEASE HORMONE (BY SIMILARITY).

- SENBELLULAR LOCATION: SECRETED (BY SIMILARITY).

- TISSUE SPECIFICITY: EXPRESSED THROUGHOUT THE BRAIN WITH HIGHEST

- LEVELS OF EXPRESSION IN MEDIAL PALLIUM, BASAL FOREBRAIN, PREOPTIC

ARBA, MIDBRAIN TEGMENTUM AND TRIGEMINAL NUCLEUS.

- SIMILARITY: BELONGS TO THE NPY / PPY / PYY PAMILY.

EMBL, APIG7559; AAD48033.1; - BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21184972; PubMed-11287086; Ebersole T.J., Conlon J.M., Goetz F.W., Boyd S.K.; Conlon J.M., Goetz F.W., Boyd S.K.; "Characterization and distribution of neuropeptide Y in the brain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INIGETPO; IPR00159; Pancreatic_hormn.
Pfam; PF00159; hormone3; 1.
PRINTS; PR00278; PANCHORMONB.
PRODOM; PD001267; PANCREATIC_hormn; 1.
PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
Neuropeptide; Cleavage on pair of basic residues; Signal; Amidation.
Neuropeptide; 1 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :: | ||||: |: | ||||: | 4 ||||: | 4 |||: | |||||: || |||||: | 4 LSGLTLALSLLV---CLGAL----AEAYPSKPDNPGDDAPAEDLARYYSALRHYINLI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., SEQUENCE OF 29-64, TISSUE SPECIFICITY, AND MASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Typhlonectes natans (Rio Cauca caecilian).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Gymnophiona, Caeciliidae, Typhlonectes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
Simmons J.M., Daniel J.A., Matteri R.L., Keisler D.H.; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.-i-SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY. EMBL, AF0957987 AAC69886.1; -. HSSP, PO1303; IRON. Interpro, IPR001955; Pancreatic_hormn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 AA; 9916 MW; 46FF2FB153EE5FFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update), 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Neuropeptide Y precursor (NPY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.8%; Score 104.5; DB 6; 10.8%; Pred. No. 0.028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 AA.
                                                                                                                                                                                                   PERM: PF00159; hormone3; 1.
PRINTS; PR00278; PANCHORMONE.
ProDom; PD001267; Pancreatic_hormn; 1.
SWART; SM001309; PAH; 1.
PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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nes 25; Conservative
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STRAIN=A3(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                        Takamatsu H., Hiraoka T., Kodama T., Koide H., Kozuka S.,
Tochikubo K., Matabe K.;
"Cloning of a novel gene yrbB, encoding a protein located in the spore integument of Bacillus subtilis.";
FEMS Microbiol. Lett. 166:361-367(1998).
EMBL; D50551; BAA24943.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 PLHIPGHTLSPAPAPAPAPARGKTGHLCSTGLDQCALGKMVPTGRYETGGLAPGHSACP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145 MDHMYHMQDQFPQQEAMSNMENANYPNMPNMPK-APEVGGVEEENVHHTVPNMPMPAVQP 203
                                                                                Gaps
                                                                                                                6 RLWLSVLTFTLSLLICLGTL.--ADAYPSKPDNPGEDAPAEDMAKYYSALRHYINLITRQR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 LEPVYPGDNATPEQMAQYAADLRRYINMLTRPRCVPQLG------REIPAPGTLG 80
                                                                                                 S RICLSLILLISTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 YYHYPAHFV---PCPVPVSPILPGSG-LCYPYYPAQAF-PMHPMHGYQPGFVSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=1902;
          BY SIMILARITY.
AMIDATION (G-65 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
                                                                                                                                                                                                                                                     Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 387;
                                                          ; Score 104; DB 13; Length 97;
; Pred. No. 0.034;
11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  387 AA; 43213 MW; F050ABF6F185DBFC CRC64;
                              (BY SIMILARITY).
9682E9D89DFFB1C7 CRC64;
                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 102.5; DB 2;
Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 CCLFPPRYGKRHKEDTL--AFSEWGSPHAAVPRELSP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEUROPEPTIDE Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative multi-domain regulatory protein. SC02259 OR SCC75A.05C. Streptomyces coelicolor.
                                                                                                                                                                                           Created)
                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                 MEDLINE=98442430; PubMed=9770294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                        11275 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%;
25.5%;
                                                            10.8%;
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06,
19,
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                                                                    Local Similarity 41.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel.
                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                             (TrEMBLrel.
  64
97
64
                                                                                                                                                                                                                                                     Bacteria, Firmicutes,
Bacillaceae, Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                          Bacillus subtilis.
                                                                                                                                                                                                                                                                                            FROM N.A.
                                       97 AA;
 23
68
64
                                                                                                                                                                                                                        YrbA protein.
                                                                                                                                                                                                    01-JUN-1998
01-DEC-2001
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                            SEQUENCE
                                       SEQUENCE
                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
PEPTIDE
PROPEP
                    MOD_RES
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                                                                      Best Loca
Matches
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Matches
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319 PAPGTAPGSSTAPPHDTASAADTAPAPGPTSAPGTAPAAGTAAPAPGTAGP--APGTSYA 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 PLEPVYPGDNATPEQMAQYAADLRRYINMLTRPRCVPQLGREIPAPGTLGPLHIPGHTLS 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Taylor K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A3(2) / M145;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.
Hopwood D.A.;
Hogwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 PAPA-----PAP-SRPALGKTGHLCSTGLDQCALGKMVPTGRYETGGLAPGHSACP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 PGTAPVAGTTPAPGTAPAPGTAGPARDTSY---APGTAPVAGTTPAPGTAPAPGSTP 430
                                                                                                                                                                                                                                                                                                                                                                  Redenbach M., Kieser H.M., Dengaite D., Bichner A., Cullum J., Kinashi H., Hopwood D.A.; As est of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1334;
                                                                                                                                                      STRAIN=A3(2);
Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.
: 78DC746883E8778C CRC64;
                                                               to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QNNYQ6
QNNYQ6, 005722, QOYS26,
QONYQ6, 005722, QOYS26,
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
-invin Flamingo 2 (DJ1163J1.1) (DJ439F8.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 102; DB 16; I
Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 417:141-147 (2002).

EMBL, AL133220, CAB61705.1;

InterPro; IPR005158; BAD.

InterPro; IPR000767; Disease_resist.

InterPro; IPR001867; Trans_reg_C.

Pfam; PF03704; BAD; 1.
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SEQUENCE FROM N.A.
MEDLINE=99308636; PubMed=10380929;
                                                                                                                                                                                                                                                                                                                                        MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00364; DISEASERSIST.
PROUTS; PR01574; TUBEXPROTEIN.
ProDom; PD000329; Trans reg_C; 1.
SEQUENCE 1334 AA; 138787 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protocadherin Flamingo 2 (DJ1163
FMI2 OR DJ1163J1.1 OR DJ439F8.2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.6%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36; Conservative
STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (NOV-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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4;

121 CGTGARLCGALCPPVP-----GGCAAAQHSALAAPTTLPACRCPPR 161

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LILLISTCVALLLOPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINMLTRPRCVPQL 69
Wu Q., Maniatis T.;
"A striking organization of a large family of human neural cadherin-
like cell adhesion genes.";
Cell 97:779-790(1999).
                                                                                        SEQUENCE FROM N.A.
MEDLINE=20202599; PubMed=10716726;
Wu Q., Manhatis T.;
"Large exons encoding multiple ectodomains are a characteristic feature of protocadherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00022; EGF_1; UNKNOWN_6.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS50227; G PROTEIN RECEP_F2; 1.
PROSITE; PS50261; G-PROTEIN_RECEP_F2_4; 1.
PROSITE; PS10248; LAMININ TYPE EGF; UNKNOWN 1..
Calcium-binding; Ccll addresion; EGF-like domain; Glycoprotein.
SEQUENCE 3014 AA; 329481 MW; C33691AD3A1DFF3A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 10.6%; Score 102; DB 4; Length 3014; Best Local Similarity 29.3%; Pred. No. 2.3; Matches 49; Conservative 9; Mismatches 63; Indels 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109 CST&LDQC-ALGKMVPTGRYETGGLAPG-HSA-----CPCCLFPPR 147
                                                                                                                                                                                                                                                                                                              Lloyd D.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP231024; AAF61930.1; -.
EMBL; AL021392; CAB50707.1; -.
EMBL; AL031588; CAB50707.1; -.
EMBL; AL031589; CAB50707.1; -.
                                                                                                                                                                                                                  SEQUENCE OF 1-1181 FROM N.A. Williams S., Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWART; SW00008; Horms; 1.
SWART; SW00282; LamG; 2.
PROSITE; PS00010; ASX HYDROXYL; UNKNOWN_2.
PROSITE; PS00232; CADHERIN 1: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR00152; Asx hydroxyl.
InterPro; IPR00126; Cadherin.
InterPro; IPR000561; BGF-11ke.
InterPro; IPR000832; GPCR_secretin.
InterPro; IPR001879; horm_receptor.
InterPro; IPR001979; haminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR000203; PKD_cys_rich.
Pfam; PP00002; 7tm_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pram; Pro0008; EGF; 6.
Pram; Pr01825; GPS; 1.
Pram; Pr02793; HRM; 1.
Pram; Pr00053; laminin EGF; 1.
Pram; Pr00054; laminin G; 1.
PRINTS; PR00205; CADHERIN.
PRINTS; PR00210; CADHERIN.
PRINTS; PR00219; GPCRSECRETIN.
PRINTS; PR0011; EGFLAMININ.
PRINTS; PR00115; CA; 9.
SWART; SM0010; EGF Lam; 1.
SWART; SM00001; EGF_like; 6.
SWART; SM00301; EGF_like; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CADHERIN 1; 6.
CADHERIN 2; 9.
                                                                                                                                                                                                                                                                                               SEQUENCE OF 1538-3014 FROM N.A.
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PROSITE; PS50268;
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"Yingwen L., Takeshi Y.;

"Yingwen L., Takeshi Y.;

"Yingwen L., Takeshi Y.;

"Daily rhythmic gene expression of neuropeptide Y in discrete brain of sering common carp. Cyprinus carpio, under the condition of self feeding.";

"Yingwen Carp. Cyprinus carpio, under the condition of self feeding.";

"Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

"I SIMILARITY: BELONGS TO THE NPY / PPY / PPY FAMILY.

"EMBL; AF287347; AAG0549.1; -...

"EMBL; AF287347; AAG0549.1; -...

"EMBL; AF287347; AAG0549.1; -...

"EMBL; PPO01309; PANCHORMONE.

"PRINTS; PRO0126; PANCHORMONE.

"PROSITE; PSS0026; PANCREATIC HORMONE.1; 1.

"PROSITE; PSS0026; PANCREATIC HORMONE.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.5%; Score 101; DB 13; Length 96; 44.9%; Pred. No. 0.062; tive 10; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 AA; 10987 MW; C6C5ABCD87688980 CRC64;
                                                                   01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                 96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: March 1, 2003, 09:13:21 Job time : 34 secs
                                 PRT;
                                                                                                                         Neuropeptide Y. Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22; Conservative
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amidation.
SEQUENCE
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                                   Q9DGK7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
RESULT 15
                29DGK7
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

US-09-965-528-16 964 1 MAAARLCLSLLLLSTCVALL......FSEWGSPHAAVPRELSPLDL 178 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

rched:

283224 cal number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
1: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		٠			SUMMARIES	
Result No.	Score	Query Match	Length	В	ΔI	Description
	441.5	45.8	95		PCHU	pancreatic hormone
8	305.5	31.7	93	~	PCDG	υ
e	260.5	27.0	100	~	B28261	
4	249.5	25.9	99	Н	PCCT	,
S	244.5	25.4	126	7	A28256	
9	236.5	24.5	96	H	PCRT	_
7	207.5	21.5	59	٦	PCSH	_
œ	186	19.3	36	~	C60071	pancreatic hormone
6	182	18.9	36	Н	C61132	pancreatic hormone
10	180	18.7	36	Н	A61132	pancreatic hormone
11	180	18.7	36	Н	D61132	pancreatic hormone
12	180	18.7	36	~	B60413	pancreatic hormone
13	177	18.4	36	Н	PCPG	pancreatic hormone
14	176	18.3	36	٦	PCBO	
15	172	17.8	36	-	B61132	pancreatic hormone
16	161	16.7	36	7	JQ0365	pancreatic hormone
17	140	14,5	93	7	I50809	peptide YY - river
18	123	12.8	36	~	A28091	pancreatic hormone
19	116	12.0	98	~	A29364	peptide YY precurs
20	114	11.8	36	7	PCFG	
21	111.5	11.6	98	7	A25916	neuropeptide Y pre
22	110.5	11.5	97	~	JC1460	×
23	110	11.4	80	٦	PCCH	pancreatic hormone
24	109	11.3	90	~	834569	YY
25	109	11.3	90	~	S34568	
56	109	11.3	97	~	S33795	Ϋ́
27	0	11.0	36	-	PCAQ	pancreatic hormone
	103.5	10.7	97	Н	NYHUY	neuropeptide Y pre
29	103	10.7	97	N	A41979	×

neuropeptide Y pre	probable multi-dom	peptide YY-related	neuropeptide Y pre	peptide YY - pig	peptide YY - human	peptide YY - dog	nonstructural poly	peptide YY precurs	spore coat protein	collagen alpha 1(I	collagen alpha 2(I	pancreatic peptide	pancreatic peptide	pancreatic peptide	nonstructural prot
150808	T50568	S26954	B41979	YYPG	A31358	A60416	MNWVRN	A55914	H69971	CGCH1S	A43291	PCGXA	PCDFY	A49743	S38480
7	~	~	~	Н	7	~	Н	7	7	Н	Н	Н	H	7	7
104	1334	37	96	36	36	36	2205	97	387	1042	1373	36	36	36	2115
10.6	10.6	10.5	10.4	10.3	10.3	10.3	10.2	10.2	10.1	10.1	10.1	10.0	10.0	10.0	9.6
102	102	101	100	66	66	66	98.5	98	97.5	97.5	97	96	96	96	95.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

	ACTUAL I
	nantrastic hormone preductor [walidated] - human
••••	
	N, Contains: pancreatic heptapeptide; pancreatic icosapeptide
	C,Species: Homo sapiens (man)
	Cidate: 17-Dec-1898 #sequence revision 25-Feb-1985 #text change 08-Dec-2000
	. d.
	J. Biol. Chem. 260, 13013-13017, 1985
	A, Title: Exons of the human pancreatic polypeptide gene, define functional domains of the
	A;Kelfefence number: A92498; MUID:86033734; PMID:2997153 A:Accession: A92408
	A; Molecule type: DNA
	A,Residues: 1-95 <lei1></lei1>
	A;Cross-references: GB:M1726; NID:19190269; PIDN:AAAA60156.1; PID:9190270
	KJUCI, D.; SUMWILZ, 1.W.; NOILIB, K.E.; FILI, N.P. EMBO J. 3. 909-912. 1984
	A, Title: A cDNA encoding a small common precursor for human pancreatic polypeptide and
	A;Reference number: A91002; MUID:84207951; PMID:6373251
	A/Accession: A9/1002
	A.Postolecute Cype: IIICAA A.Rostolecute (TPC)
	A.Cross-references: GB:X00491: NID:q35889: PIDN:CAA25161.1: PID:q35590
	R; Leiter, A.B.; Keutmann, H.T.; Goodman, R.H.
	J. Biol. Chem. 259, 14702-14705, 1984
	A; Title: Structure of a precursor to human pancreatic polypeptide.
	A, Reference number: A22587; MUID:85054955; PMID:6094571
	A/Accession: AZZS87
	A / WO1eCute Cype: mkNA A . Reacidines 1 - 95 / 1.E.T.2 .
	A;Note: part of this sequence, including the amino end of the mature protein, was detern
	R; Takeuchi, T.; Gumucio, D.L.; Yamada, T.; Meisler, M.H.; Minth, C.D.; Dixon, J.E.; Edd
	J. Clin. Invest. 77, 1038-1041, 1986
	A/Title: Genes encoding pancreatic polypeptide and neuropeptide Y are on human chromoson
	Aiketerence number: 155543; MUID:86140/15; PMID:3753985
	A.Status: 1.0130 A.Status: preliminary: translated from CR/EMBI./DDB.T
	A; Molecule from many / molecule from molecu
	A;Residues: 1-85,'I',87-95 <tak1></tak1>
	A;Cross.references: GB:M15788; NID:g190301; PIDN:AAA60161.1; PID:g190302
	Njakeucil, 11, Zamada, 1. Proc. Natl. Acad. Kri II & A 2 1536-1539 1985
	A,Title: Isolation of a CDNA clone encoding parcreatic polypeptide.
	A;Reference number: A94026; MUID:85140331; PMID:3856278
	A/Accession: A94026
	A; Molecule type; mRNA A; no. 1 or : 1 or : mnvo.
	A, Kebiddes I - 20, I., 5, 79 s. (1947.) R. Schwartz, T. W. Hansen, H. F. Hakanson, R. Gundler, B. Tarar, H. G.
	Proc. Natl. Acad. Sci. U.S.A. 81, 708-712, 1984
	A; Title: Human pancreatic icosapeptide: isolation, sequence, and immunocytochemical loca
_	A;Reference number: A94018; MUID:84144773; PMID:6366786

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A;Accession: A26073
A;Molecule type: protein
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Best Local Similarity
Matches 58; Conserv
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A; Residues: 1-100 <YON>
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A; Residues: 1-93 <TOO>
A; Residues: 1-93 <TOO>
A; Residues: 1-93 <TOO>
A; Cross-references: GB: M35596; NID:g164049; PIDN: AAA10886.1; PID:g164050
A; Cross-references: GB: M35596; NID:g164049; PIDN: AAA10886.1; PID:g164050
B; Chance; R.E.; Johnson, M.G.; Hoffmann, J.A.; Jones, W.E.; Koffenberger Jr., J.E.
R; Chance, R.E.; Johnson, M.G.; Hoffmann, J.A.; Jones, W.E.; Roffenberger Jr., J.E.
San Francisco, and London, 1979
A; Reference number: A94465
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NyContains: pancreatic polypeptide cissapeptide
C;Species: Canis lupus familiaris (dog)
C;Date: 25.Feb-1985 #sequence_revision 12.Apr-1996 #text_change 18-Jun-1999
C;Accession: A40904; A94465; A93270; A01567
C;Accession: P.; Paquette, T.L.
Endocrinol. 1, 413-419, 1987
Litle: Canine pancreatic polypeptide complementary deoxyribonucleic acid sequence: pan A;Reference number: A40904; MUID:90331935; PMID:3079195
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A;Residué§: 69-88 <SCH>
C;Comment: The hormone precursor molecules are stored in islet cells of the duodenal pan
C;Superfamily: pancreatic hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;1-29/Domain: signal sequence #status predicted <SIG>
;30-65/Product: pancreatic hormone #status predicted <PCH>
;69-88/Product: pancreatic icosapeptide #status experimental <PCI>
9-95/Product: pancreatic heptapeptide #status predicted <PCI>
5/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following 91)
                          A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Residues: 69-88 < SCH>
R; A; Molecule type: J3, 275-285, 1991
A; Title: Patterns of immunoreactive pancreatic polypeptide in human plasma.
A; Reference number: A60068; MUID: 91352354; PMID: 1882090
A; Reference number: A60068; MUID: 91352354; PMID: 1882090
A; Molecule type: protein
A; Molecule type: 
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A;Residues: 30-65 <CHA>
R;Schwartz, T.W.; Tager, H.S.
Nature 294, 589-591, 1981
A;Title: Isolation and biogenesis of a new
A;Reference number: A93270; MUID:82080694;
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Best Local Similarity
Matches 95; Conserv
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A; Accession: A94018
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pancreatic hormone precursor - cat (tentative sequence) (fragment)
NyAlternate names: pancreatic polypeptide precursor
NyAlternate names: pancreatic polypeptide precursor
NyContains: pancreatic hormone; pancreatic icosapeptide
C;Species: Felis silvestris catus (domestic cat)
C;Accession: Az6073
R;Nielsen, H.V.; Gether, U.; Schwartz, T.W.
Biochem, J. 240, 69-74, 1986
A;Title: Cat pancreatic elcosapetide and its biosynthetic intermediate. Conservation c
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C;Species: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
C;Accession: B28261
R;Yonekura, H.; Nata, K.; Watanabe, T.; Kurashina, Y.; Yamamoto, H.; Okamoto, H.
D Biol, Chem. 263, 2996-2997, 1988
A;Title: Mosaic evolution of prepropancreatic polypeptide. Structural conservation and A;Reference number: A92708; MUID:88139354; PMID:3343236
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C,Keywords: amidated carboxyl end; hormone; pancreas
F;1-20/Domain: signal sequence #status predicted <SIG>F;30-65/Product: pancreatic hormone #status experimental <PCH>F;69-88/Product: pancreatic icosapeptide #status experimental <PCI>F;69-88/Product: pancreatic icosapeptide #status experimental <PCI>F;65/Modified site: amidated carboxyl end (Tyr) (amide in mature form from :
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                                                                                                                                                                                                                                                                                                                                                                  Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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N'Contains: pancreatic hormone; pancreatic icosapeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.0%; Score 260.5; DB 2 61.1%; Pred. No. 9.7e-14; iive 5; Mismatches 25
                                                                                                                                                                                                                                                                                                                                                            Query Match 31.7%; Score 305.5; DB 1
Best Local Similarity 40.5%; Pred. No. 2.8e-17;
Matches 70; Conservative 5; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRPR----YGKRAEEENTGG---LPGVQLSPCTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic hormone precursor - mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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A; Accession: A28261
A; Molecule type: DNA
A; Residues: 1-98 «YON»
A; Cross-references: GB:M18207; GB:J03543; NID:g206325; PIDN:AAA41922.1; PID:g206326
A; Cross-references: GB:M18207; GB:J03543; NID:g206325; PIDN:AAA41922.1; PID:g206326
A; Cross-references: GB:M18207; GB:J03543; NID:g206325; PIDN:AAA41922.1; PID:g206326
A; Title: Different splice site utilization generates diversity between the rat and human A; Reference number: S06472; MUID:89104395; PMID:3214179
A; Accession: S06472
A; Accession: S06472
A; Molecule type: DNA
A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Superfamily: pancreatic hormone
C,Keywords: amidated carboxyl end; hormone; pancreas
C;Reywords: amidated carboxyl end; hormone; predicted <SIG>
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-65/Product: pancreatic icosapeptide #status predicted <PCI>
F;65/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gl);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pancreatic hormone precursor - sheep (tentative sequence) (fragment)
N;Alternate names: pancreatic polypeptide precursor
N;Contains: pancreatic hormone; pancreatic icosapeptide
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 31-Mar-2000
C;Accession: B94465; A9132; A01569
R;Chance, R.E.; Johnson, M.G.; Hoffmann, J.A.; Jones, W.E.; Koffenberger Jr., J.E.
unpublished results, cited by Chance, R.E., Moon, N.E., and Johnson, M.G., in Methods on San Francisco, and London, 1979
                                                                                                                                                                                                                                   rat and human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Comment: We have added, by homology with the human precursor sequence, Gly-37, which C;Superfamily: panoreatic hormone C;Keywords: amidated carboxyl end; hormone; pancreas P:1-36/Product: panoreatic hormone #status experimental <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Title: Isolation of ovine pancreatic icosapeptide: a peptide product containing one A,Reference number: A91323, MUID:84208777, PMID:6723953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAVAYYCLSLFLLSTWVALLLQPLQGAWGAPLEPMYPGDYATHEQRAQYETQLRRYINTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-98 <YAM>
A;Cross-references: GB:M13588; NID:g206327; PIDN:AAA41923.1; PID:g206328
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TRPR----YGKR--DEDTAG---LPGRQLPP---------------CTSLLVGLMPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 236.5; DB 1
Pred. No. 7.1e-12;
6; Mismatches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24.5%;
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A,Residues: 1-36 <CHA>
R,Schwartz, T.W.; Hansen, H.F.
FEBS Lett. 168, 293-298, 1984
A,Title: Isolation of ovine pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Accession: B94465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 LGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-66 <NIE>
C;Comment: We have added, by homology with the human precursor sequence, Gly-37, which is C;Superfamily: pancreatic hormone
C;Superfamily: pancreatic hormone
C;Keywords: amigated carboxyl end, hormone; pancreas
F;1-36/Product: pancreatic hormone #status experimental <PCH>
F;1-36/Product: pancreatic icosapeptide #status experimental <PCH>
F;36/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
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N.Gontains: pancreatic polypeptide precursor
N.Gontains: pancreatic hormone; pancreatic icosapeptide
C.Species: Rattus incrvegicus (Norway rat)
C.Species: Rattus incrvegicus (Norway rat)
C.Species: 30-Jun-1987 #sequence revision 30-Jun-1987 #text_change 18-Jun-1999
C.Accession: A28261; S06472; Ā01571
C.Species: A.Y. Watca. K.; Watcanabe, T.; Kurashina, Y.; Yamamoto, H.; Okamoto, H.
J. Biol. Chem. 263, 2990-2997, 1988
A.Title: Mosaic evolution of prepropancreatic polypeptide. Structural conservation and A.Reference number: A92708; MUID:88139354; PMID:3343236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pancreatic hormone precursor - guinea pig
N'Alternate names: pancreatic polypeptide precursor
N'Contains: pancreatic hormone: pancreatic icosapeptide
C'Species: Cavia porcellus (guinea pig)
C'Date: 30-Jun.1989 #sequence_revision 30-Jun-1989 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 SPAPAPAPSRPALGKTGHLCSTGLDQCALGKMVPTGRYETGGLAPGHSACPCCLFPPRYG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                        30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPRCVPQLGREIPAPGTLGPLHIPGHTL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----PRYG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRPR----YGKSAEEDALGLPVWRQSHAAAPGGSHRHPPAGLPA--AKGGTG 103
                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Indels
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                                                                                                                                                                                                                                                                                              Score 249.5; DB 1 Pred. No. 4.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 APLEPVYPGDNATPEQMAQYAAELRRYINMLTR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 KRHKEDTLAFSEWGSPHAAVPRELSPLDL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pancreatic hormone precursor - rat
                                                                                                                                                                                                                                                                                              25.9%;
36.9%;
                                                                                                                                                                                                                                                                                                                                                                     55; Conservative
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C,Accession: A61132
R;Henry, U.S.; Lance, V.A.; Conlon, U.M.
Renry, U.S.; Lance, V.A.; Conlon, U.M.
A;Title: Primary structure of pancreatic polypeptide from four species of perissodactyl?
A;Title: Primary structure of pancreatic polypeptide from four species of perissodactyl?
A;Reference number: A61132; MUID:92225314; PMID:1808025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pancreatic hormone - Przewalski's horse
NyAlternate names: pancreatic polypeptide
NyAlternate names: pancreatic polypeptide
CySpecies: Bquus caballus przewalskii (Przewalski's horse)
CyBate: 12-Mar-1994 #sequence_revision 07-Oct-1994 #text_change 26-Feb-1999
CyAccession: D61132
RiHenry, J.S.; Lance, V.A.; Conlon, J.M.
Gen. Comp. Endocrinol. 84, 440-446, 1991
A;Title: Primary structure of pancreatic polypeptide from four species of perissodactyl.
A;Reference number: A61132; MUID:92225314; PMID:1808025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description hormone - Chinchilla brevicaudata
NyAlternate names: pancreatic polypeptide
C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C;Species: Chinchilla brevicaudata, Chinchilla lanigera brevicaudata
C;Date: 03-Feb-1993 #equence_revision 03-Feb-1993 #text_change 12-Apr-1995
C;Accession: B60413
R;Eng. J.; Klaiman, W.A.; Chu, L.S.
Peptides 11, 683-685, 1990
A;Title: Purification of peptide hormones from chinchilla pancreas by chemical assay.
A;Accession: B60413; MUID:91045327; PMID:2235678
A;Status: preliminary
                                                                                                                                                                                                                                                                      N.Alternate names: pancreatic polypeptide
C;Species: Equus zebra (mountain zebra)
C;Date: 10-Mar-1994 #sequence_revision 07-Oct-1994 #text_change 26-Feb-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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C.Keywords: amidated carboxyl end; hormone; pancreas
Fp.1-36/Product: pancreatic hormone #status experimental <PCH>
F;1-36/Productic amidated carboxyl end (Tyr) #status experimental
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C;Keywords: amidated carboxyl end; hormone; pancreas
F;1-36/Product: pancreatic hormone #status experimental <PCH>
F;36/Modified site: amidated carboxyl end (Tyr) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.7%; Score 180; DB 1; L
llarity 94.3%; Pred. No. 6.9e-08;
Conservative 2; Mismatches 0;
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llarity 94.3%; Pred. No. 6.9e-08;
Conservative 2; Mismatches 0;
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1 APLEPVYPGDNATPEQMAQYAAELRRYINMLTRPR
                                                                                                                                                                                                                                      pancreatic hormone - mountain zebra
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hes 33; Conserv
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Best Local Similarity
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NyAlternate names: pancreatic polypeptide

Syspecies: Tapirus pinchaque (mountain tapir)

Cybecies: Tapirus pinchaque (mountain 07-Oct-1994 #text_change 26-Feb-1999

Cybecies: Comp. Endocrinol. 84, 440-446, 1991

A;File: Primary structure of pancreatic polypeptide from four species of perissodactyla

A;Reference number: A61132, MUD:9225314; PMID:1808025

A;Accession: C61132

A;Reference number: A61132

A;Reference number:
       F;40-59/Product: pancreatic icosapeptide #status experimental <PCI>
F;36/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 relationship to human sequences.
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C;Species: Macaca mulatta (rhesus macaque)
C;Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 15-Jun-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                     90 SPAPAPAPSRPALGKTGHLCSTGLDQCALGKMVPTGRYETGGLAPGHSACPCCLFPPRYG 149
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A;Nolecule type: protein
A;Residues: 1-36 < YUA>.
A;Residues: 1-36 < YUA>.
A;Note: the sequence is identical with the human sequence
C;Superfamily: pancreatic hormone
C;Keywords: amidated carboxyl end; hormone; pancreas
F;36/Modified site: amidated carboxyl end (Tyr) #status experimental
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R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.
Regul. Pept. 32, 39-45, 1991
A;Title: Rhesus monkey gastroenteropancreatic hormones: A;Reference number: A60071; MUID:91164506; PMID:2003150
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                                                                                                                               DB 1;
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                                                                                                                           Score 207.5; DB 1
Pred. No. 7.9e-10;
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                                                                                                                                                                                                  2; Mismatches
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                                                                                                                           21.5%;
ilarity 35.2%;
Conservative
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Best Local Similarity 100.0
Matches 35; Conservative
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Best Local Similarity 97.19
Matches 34; Conservative
                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chance, R.E.; Johnson, M.G.; Hoffmann, J.A.; Lin, T.M.
in Proinsulin, Insulin, C-Peptide, Baba, S., Kaneko, T., and Yanaihara, N., eds., pp.419
A;Reference number: A01568
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N;Alternate names: pancreatic polypeptide
C;Species: Ceratotherium simum (white rhinoceros, square-lipped rhinoceros)
                                                                                                                                                                                                                                                                                                                                                                                       N;Alternate names: pancreatic polypeptide
C;Species: Sus scrofa domestica (domestic pig)
Pate: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 23-Aug-1996
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C.Keywords: amidated carboxyl end, hormone; pancreas
F:1-15-Product: pancreatic hormone #status experimental <PCH>
F:36/Modified site: amidated carboxyl end (Tyr) #status experimental
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A;Molecule type: protein
A;Residues: 1-36 <CHA>
C;Superfamily: pancreatic hormone
C;Keywords: amidated carboxyl end; hormone; pancreas
F;1-36/Product: pancreatic hormone #status experimental <PCH>
F;36/Modified site: amidated carboxyl end (Tyr) #status experimental
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Pred. No. 1.4e-07;
1; Mismatches 1; Indels
                                                                                            Length 36;
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                                                                                                                                             0; Indels
                                                                                            ch 18.7%; Score 180; DB 2; 1 Similarity 94.3%; Pred. No. 6.9e-08; 33; Conservative 2; Mismatches 0;
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                       A, Residues: 1-36 < ENG>
C, Superfamily: pancreatic hormone
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A; Molecule type: protein A; Residues: 1-36 < ENG>
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Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
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Best Local Similarity
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C; Date: 10-Mar-1994 #sequence_revision 07-Oct-1994 #text_change 26-Feb-1999
C; Accession: B61132
R; Henry, J.S.; Lance, V.A.; Conlon, J.M.
Gen. Comp. Endocrinol. 84, 440-446, 1991
A; Title: Primary structure of pancreatic polypeptide from four species of perissodactyl A; Title: Primary structure of pancreatic polypeptide from four species of perissodactyl A; Mcdecule type: Drotein
A; Reference number: A61132, MUID:92225314; PMID:1808025
A; Accession: B61132
A; Accession: B61132
A; Mcdecule type: protein
A; Residues: 1.36 cHBN.
C; Superfamily: pancreatic hormone
C; Keywords: amidated carboxyl end; hormone; pancreas
C; Keywords: amidated carboxyl end (Tyr) #status experimental
C; Keywords: amidated carboxyl end (Tyr) #status experimental
C; Modified site: amidated carboxyl end (Tyr) #status experimental
Cuery Match
Best Local Similarity 91.4%; Pred. No. 2.9e-07;
Matches 32; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Cy 30 APLEPVYPGDNATPEDMAQYAADLRRYINMLTRPR 64
1: Indels 0; Stabs 0;
Db 1: SplePVYPGDNATPELMAQYAABLRRYINMLTRPR 35
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

March 1, 2003, 09:11:12 ; Search time 12 Seconds
 (without alignments)
 615.232 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-965-528-16 964 1 MAARLCLSLLLLSTCVALL......FSEWGSPHAAVPRELSPLDL 178

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues rched:

al number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	ption	98 homo sapien	bos t	99 canis famil	_	84 felis silve	83 cavia porce		01 ovis aries	84 macaca mula			00 equus zebra	00 sus scrofa	99 ceratotheri		36 oryctolagus		98 lampetra fl			d3 ictalurus p	29 rana tempor	s2 mus musculu	74 mus musculu			06 gallus gall				2	96	p3 brachydanio
	Desc	P01298	P01302	P01299	P10601	P06884	P13083	P06303	P01301	P33684	P39659	P41519	P38000	P01300	P379	P41335	P41336	P18107	P48098	P15427	P10631	Q9 i 9d3	P31229	Q9eps2	P57774	P07808	P33689	P013	P10082	Q9i8p2	09pt 98	P06305	09pt 9	0918
SUMMARIES		IUMAN	BOVIN	CANFA	10USE	FELCA	CAVPO	RAT	SHEEP	MACMU	TAPPI	CHIBR	EQUZE	O_PIG	CERSI	J_ERIEU	RABIT	DIDMA	AMFL	SANCA	T.	ICTPU	RANTE	OUSE	10USE	RAT	XENLA	CHICK	HUMAN	BRARE	SLA	ALLMI	DICLA	BRARE
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de	Query Match	45.8	36.3	31.7	•	25.9	25.4	24.5	21.5	19.3	18.9	18.7	18.7	18.4			7.	16.7		12.8				11.8	•	•	•	•	11.3		•	11.0	11.0	10.8
	Score	441.5	349.5	305.5	260.5	249.5	244.5	236.5	207.5	186	182	180	180	177	176	173	167	161	140	123	116	115.5	114	113.5	111.5	111.5	110.5	110	109	108	107	106	106	104.5
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NEUY_HUMAN NEUY_CHICK NEUY_DICLA NEUY_LAMFL CLRI HUMAN PYY_RAJRH PYY_RAJRH PYY_CHICK NEUY_CARAU PYY_PIG	CA11_CHICK
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97 99 104 3014 36 37 2205	1453
011001100100100100100100100100100100100	10.1
103,5 102.5 102.5 102 101 101 100 99	97.5
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4 45

ALIGNMENTS

STANDARD; PRT; 95 AA.		Pancreatic hormone precursor (Pancreatic polypeptide) (PP). PPY OR PNP.	Chordata;	ia, Primates, Catarrhini		N.A. 951; PubMed=6373251;	T.W., Norris K.E., Fiil	ing a small common precursor for human pancreatic and pancreatic icosapeptide.";	EMBO J. 3:909-912(1984).	N.A.	MEDLINE=86033734; PubMed=2997153; Leiter & B. Montminy M.D. Jamieson F. Goodman D.H.:	eatic polypeptid	of the precursor.";	Biol. Chem. 260:13013-13017(1985).	N.A.	MEDLINE=85054955; PubMed=60945/1; Leiter A.B., Keutmann H.T., Goodman R.H.;	a precursor to human pancreatic polypeptide.";	. 259:14702-14705(1984).	N.A.	PubMed=3753985;	T., Gumucio D.L., Yamada T., Meisler M.H., Minth C.D., 3 Eddv R.E Shows T.B.:	ng pancreatic polypeptide and neuropeptide Y are on	Nan Chromosomes 17 and 7.";		9-88. 773. DitMed-636786.	undler F.,	atic icosapeptide: isolation, sequence, and nical localization of the cook-terminal fragment of the	1	FIGS: NACI: ACAG: SCI: U.S.A. BI:/UB-/12(1984). -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS	OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND GASTROLIMITESTINAL RINGTIONS	SECTION: THE PHYSICAL ROLE FOR THE ICOSAPEPTIDE HAS	LOCATION: Secreted.	
AN O HUMAN	21-JUL-1986 (Rel. 21-JUL-1986 (Rel. 16-OCT-2001 (Rel.	Pancreatic hormore PPY OR PNP.	Homo sapiens (Human) Eukaryota; Metazoa;	Mammalia; Euther	[1]	SEQUENCE FROM N.A. MEDLINE=84207951;	Boel E., Schwartz	"A cDNA encoding polypeptide and	ЕМВО J. 3:909-91	SEQUENCE FROM N.A.	MEDLINE=86033734	"Exons of the hu	domains of the p	J. Biol. Chem. ? [3]	SEQUENCE FROM N.A.	MEDLINE=85054959 Leiter A.B., Keu	"Structure of a	Biol. Chem.	14) SEQUENCE FROM N.A.	MEDLINE=86140719	Takeuchi T., Gur Dixon J.E Eddy	"Genes encoding	human chromosome	[5]	SEQUENCE OF 69-8	Schwartz T.W., F	"Human pancreati	pancreatic poly	Froc. Natl. Acad	OF LANGERHAN	-!- FUNCTION: TE		-!- SIMILARITY:
RESULT 1 PAHO HUM ID PAH	25.5	S E	8 လ	88	Z.	RP XX	RA	RT	RI.	RP	ZX g	RT	RŢ	R. RN	RP	X X	RT	Z Z	R R P	KX E	¥ 2	RT	RT PI.		RP		RT			ខ្លួ	ខម	388	ນ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 441.5; DB 1; Length 95;
Pred. No. 2e-27;
0; Mismatches 0; Indels 83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION (G-66 PROVIDE AMIDE GROUP). 
 V -> I (IN REF. 4). 
 44F0265092F9C4A0 CRC64;
                                                                                                                                                                                                                                                                                                                                PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
Hormone; Cleavage on pair of basic residues; Pancreas; Signal; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
1-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone precursor (Pancreatic polypeptide) (PP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE=95132646; PubMed=7831336;
MEDLINE=9132646; Submeider R., Shine J.;
Merzog H., Hort Y., Schneider R., Shine J.;
"Sæninalpiasmin: recent evolution of another member of the newropeptide Y gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                       PANCREATIC HORMONE.
PANCREATIC ICOSAPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         newropeptide Y gene family.";
Proc. Natl. Acad. Sci. U.S.A. 92:594-598(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 131 AA
                                                                                                                                                                                                                                                                         InterPro; IPR001955; Pancreatic_hormn.
                                                                                                                                                                                                                                                                                       Pfam; PF00159; hormone3; 1.
PRINTS; PR00278; PANCHORMONE.
SMART; SM00309; PAH; 1.
                                                                                                                                           EMBL; X00491; CAA25161.1; -. EMBL; M11726; AAA60156.1; -. EMBL; M15788; AAA60161.1; -.
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95; Conservative
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Genew; HGNC:9327; PPY.
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PIR; A22587; A22587.
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CONFLICT
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Matches 9
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PAHO_BOVIN
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                                                                                                                                                                                                                             bovine paracratic polypeptide.",
Biochmistry 31:1245-1253(1992).
-!- FUNCTION: PANCREATIC FORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
GASTROINTESTINAL FUNCTIONS.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- SUBCELLUIAR BELONGS TO THE NPY / PPY PAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-66 PROVIDE AMIDE GROUP).
                                                                                                                                       [3]
STRUCTURE BY NMR.
MEDLINE=92135211; PubMed=1734969;
Li X., Sutcliffe M.J., Schwartz T.W., Dodson C.M.;
Li X., Sutcliffe M.J., Schwartz T.W., Dodson C.M.;
"Sequence-specific IH NMR assignments and solution structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMARY; SM0309; PAH; 1.
PROSITE; PS00265; PANCREATIC HORMONE 1; 1.
PROSITE; PS50276; PANCREATIC HORMONE 2; 1.
Hormone; Cleavage on pair of basic residues; Pancreas; Signal;
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C-TERMINAL PEPTIDE 2 (POTENTIAL)
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21-UUL-1986 (Rel. 01, Created)
01-NOV-1990 (Rel. 16, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone precursor (Pancreatic polypeptide) (PP).
Chance R.E., Johnson M.G., Hoffmann J.A., Jones W.E., Koffenberger J.E. Jr.;
Unpublished results, cited by:
Unpublished R.E., Moon N.E., Johnson M.G.;
(In) Jaffe B.M., Behrman H.R. (eds.);
Methods of hormone radioimmunoassay (2nd ed.), pp.657-672, Academic Press, New York and London (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14375 MW; DCDFE1011C67DF9B CRC64;
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Pred. No. 2.7e-20;
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PDB; 1BBA; 31-0CT-93.
InterPro; IPR001955; Pancreatic_hormn.
Pfam; PF00159; hormone3; 1.
PRINTS; PR00278; PANCHORMONE.
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48.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished results, cited by:
Whislaen H.V., Geblar U., Schwartz T.W.;
Biochem. J. 240:69-74(1986).
-!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-82080694; PubMed=7031480;
Schwartz T.W., Tager H.S.;
"Isolation and biogenesis of a new peptide from pancreatic islets.";
Nature 294:589-591(1981):
                                                                                                                                   Toochman P., Paquette T.L.,
Toochman P., Paquette T.L.,
"Canine pancreatic polypeptide complementary deoxyribonucleic acid
sequence: pancreatic polypeptide and insulin messenger ribonucleic
acid distribution in the lobes of the pancreas.";
Mol. Endocrinol. 1:413-419(1987).
                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION (G-66 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00265; PANCREATIC HORMONE 1; 1.
PROSITE; PS50276; PANCREATIC HORMONE 2; 1.
Hormone; Cleavage on pair of basic residues; Pancreas; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS NOT YET BEEN ELUCIDATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 305.5; DB 1; Length 93;
Pred. No. 4.3e-17;
5; Mismatches 15; Indels 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND GASTROINTESTINAL FUNCTIONS.
                                                                                                                                                                                                                                                              Chance R.E., Johnson M.G., Hoffmann J.A., Jones W.E.,
Koffenberger J.E. Jr.;
Unpublished results. cited by:
Chance R.E., Moon N.E., Johnson M.G.;
(In) Jaffe B.M., Behrman H.R. (eds.);
Methods of hormone radioimwinoassay (2nd ed.), pp.657-672,
Academic Press, New York and London (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B88D6D1F0281F413 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PANCREATIC HORMONE.
PANCREATIC ICOSAPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001955; Pancreatic hormn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87156600; PubMed=3827854;
Schwartz T.W.;
                                                                                                                        MEDLINE=90331935; PubMed=3079195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00278; PANCHORMONE. SMART; SMO0309; PAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10427 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M35596; AAA30886.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 40.5°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00159; hormone3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
88
93
               Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A01567; PCDG.
A40904; A40904.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01302; 1BBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEOUENCE OF 89-93.
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 69-88.
                                                                                                                                                                                                                                                    SEQUENCE OF 30-65
                                                                 _TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amidation.
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SEQUENCE
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1;

Gaps

83;

40.5%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
                                                                  61 TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPPAPSRPALGKTGHLCSTGLDQCALGK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conservation and divergence in pancreatic polypeptide gene.";
J. Biol. Chem. 263:2990-2997(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MAAARLCLSLILLSTCVALILOPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                                                                                                        62
1 MAAARLCLSLLLLSTCVALLLQPLLGAQGAPLEPVYPGDNATPEQMAQYAADLRRYINML 60
                   1 MPAACRCLFLLLLSACVALLLQPPLGTRGAPLEPVYPGDDATPEQMAQYAAELRRYINML 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (G-66 PROVIDE AMIDE GROUP).
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PROSITE; PSS0276; PANCREATIC HORMONE 2; 1.
Hormone; Amidation; Pancreas; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Okamoto H.; "II. Structural "Mosaic evolution of prepropancreatic polypeptide." II. Structural
                                                                                                                                         121 MVPTGRYETGGLAPGHSACPCCLFPPRYGKRHKEDTLAFSEWGSPHAAVPREL 173
                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-88139354; PubMed=3343236;
Yonekura H., Nata K., Watanabe T., Kurashina Y., Yamamoto H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 100;
                                                                                                                                                                                                                                                                                                                      01-JUL-1989 (Rel. 11, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone precursor (Pancreatic polypeptide) (PP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND GASTROINTESTIMAL FUNCTIONS. SUBCELLULAR LOCATION: Secreted. SIMILARITY: BELONGS TO THE NPY / PPY / PYX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 29 PANCREATIC HORMONE.
30 65 C-TERMINAL PEPTIDE.
69 100 C-TERMINAL PEPTIDE.
65 65 AMIDATION (G-66 PROVIDE AI
100 AA; 11020 MW; AODODO4FB7DFB9D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 260.5; DB 1;
Pred. No. 1.2e-13;
5; Mismatches 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001955; Pancreatic_hormn.
Pfam; PF00159; hormone3; 1.
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00278; PANCHORMONE.
SMART; SM00309; PAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M18208; AAA39967.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 61.1%;
58; Conservative
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                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P01302; 1BBA.
MGD; MGI:97753; Ppy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B28261; B28261.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                               PAHO MOUSE
P10601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                             polypeptide precursor.";
J. Biol. Chem. 263:2911-2916(1988).
-!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
GASTROINTESTINAL FUNCTIONS.
-!- FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS
NOT YET BEEN ELUCIDATED.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Bukarayota, Metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae, Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PANCREATIC HORMONE.
PANCREATIC TOCASAPEPTIDE.
AMIDATION (G-63 PROVIDE AMIDE GROUP).
76C1311560F566326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MTATRCCLWLLLLGTCMALLLPE---AWGAPLEPVYPGDDATPQQMAQYAAEMRRYINML
                                                                                                                      Cavia porcellus (Guinea pig).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                     MEDINE=88139344; PubMed=2830269;
Blackstone C.D., Seino S., Takeuchi T., Yamada T., Steiner D.F.;
"Novel organization and processing of the guinea pig pancreatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M29543; AAA37051.1; -
PIR; A28256; A28256.
InterPro; 1PR001955; Pancreatic_hormn.
Pfam; PF00159; hormone3; 1.
PRINTS; PR00278; PAHCHORMONE.
SMART; SM00309; PAH; 1.
PROSTIFF; PS00276; PANCREATIC_HORMONE_1; 1.
PROSTIFF; PS00265; PANCREATIC_HORMONE_2; 1.
Hormone; Cleavage on pair of basic residues; Pancreas; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRPR----YGKSAEEDALGLPVWROSHAAAPGGSHRHPPAGLPA--AKGGTG 103
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U-JAN-1988 (Rel. 06, Last sequence update)
15.JUN-2002 (Rel. 41, Last annotation update)
Pancreatic hormone precursor (Pancreatic polypeptide) (PP).
01-JAN-1990 (Rel. 13, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone precursor (Pancreatic polypeptide) (PP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 244.5; DB 1; Length
Pred. No. 2.4e-12;
9; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 AA.
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62
126
62
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                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI TaxID=10141;
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27
67
62
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A Nielsen H.V. Gether U., Schwartz T.W.;

Mielsen H.V. Gether U., Schwartz T.W.;

I cat pancreatic elcosapeptide and its biosynthetic intermediate.

Conservation of a monobasic processing site.";

Elochem. U. 240:69-74(1986).

Elochem. U. 240:69-74(1986).

C. - FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS

C. - FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS

C. - FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS

NOT YET BERN ELUCIDATED.

C. - SUBCELLULAR LOCATION: Secreted.

- MISCELLALELANDENCES GLY-LYS-ARG AT POSITIONS 37 TO 39 WERE INCLUDED BY HOMOLOGY WITH OTHER PANCREATIC HORMONE TYPE PRECURSOR SEQUENCE.

- SIMILARITY: BELONGS TO THE NPY / PYY FAMILY.
                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone precursor (Pancreatic polypeptide) (PP) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 SPAPAPAPSRPALGKTGHLCSTGLDQCALGKMVPTGRYFTGGLAPGHSACPCCLFPPRYG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
      1 MAVAYCCLSLFLVSTWVALLLQPLQGTWGAPLEPMYPGDYATPEQMAQYETQLRRYINTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPRCVPQLGREIPAPGTLGPLHIPGHTL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 APLEPVYPGDNATPEQMAQYAAELRRYINMLTR------33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----- PRYG 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PANCREATIC HORMONE.
PANCREATIC ICOSAPEPTIDE.
AMIDATION (G-37 PROVIDE AMIDE GROUP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Felis silvestris catus (Cat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Carnivora, Pissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00265; PANCREATIC HORMONE 1; 1.
PROSITE; PSS0276; PANCREATIC HORMONE 2; 1.
Hormone; Amidation; Pancreas; Cleavage on pair of basic residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 249.5; DB 1; Length 66; Pred. No. 5.6e-13; 5; Mismatches 6; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2D3A94BD9063A83D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                                                 66 A.A.
                                                              61 TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAP 95
                                                                                                                      61 TRPR----YGKRAEBENTGG---LPGVOLSPCTSP 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126
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HSSP, P01302; 1BBA.
InterPro; IPR001955; Pancreatic_hormn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 KRHKEDTLAFSEWGSPHAAVPRELSPLDL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
PAHO CAVPO
ID PAHO CAVPO STANDARD; P
AC P13083;
DT 01-JAN-1,990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7483 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00159; hormone3; 1.
SMART; SM00309; PAH; 1.
                                                                                                                                                                                                                                                   .
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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36
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Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9685;
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                                                                                                                                                                                                                                                                          FELCA
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Hormone; NON TER PEPTIDE PEPTIDE MOD_RES NON_TER SEQUENCE

Query Match

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SEQUENCE

P06884;

OC OC GEN DIT OF OC

PAHO

RESULT 5 PAHO FELCA

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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone precursor (Pancreatic polypeptide) (PP) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SUBCELLULAR LOCATION: Secreted.
-:- MISCELLANDEDUS: GLY-LYS-ARG AT POSITIONS 37 TO 39 WERE INCLUDED BY
HOMOLOGY WITH OTHER PANCREATIC HORMONE TYPE PRECURSOR SEQUENCE.
-:- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 SPAPAPAPSRPALGKTGHLCSTGLDQCALGKMVPTGRYETGGLAPGHSACPCCLFPPRYG 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE 84208777; PubMed=6723953; Schwartz T.W., Hansen H.F.; Schwartz T.W., Hansen H.F.; Schwartz T.W., Hansen H.F.; "Isolation of ovine pancreatic icosapeptide: a peptide product containing one cysteine residue."; FEBS Lett. 168:293-298(1984).
-!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND GASTROINTESTINAL FUNCTIONS.
-!- FUNCTION: THE PHYSIOLOGICAL ROLE FOR THE ICOSAPEPTIDE HAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 83; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPRCVPQLGREIPAPGTLGPLHIPGHTL 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ASLEPEYPGDNATPEQMAQYAAELRRYINMLTR---------33
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                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hormone; Cleavage on pair of basic residues; Amidation; Pancreas.
NON TER 1 36 PANCREATIC HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PANCREATIC ICOSAPEPTIDE.
AMIDATION (G-37 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.5%; Score 207.5; DB 1; Length 59; 35.2%; Pred. No. 7.8e-10; ive 2; Mismatches 7; Indels 83
                                                                                                                                                                                                                                                                                                                                                                                             Chance R.E., Johnson M.G., Hoffmann J.A., Jones W.E., Koffenberger J.B. Jr., Unpublished results, Cited by: Chance R.E., Moon N.E., Johnson M.G.; Chance R.E., Moon N.E., Johnson M.G.; Methods of hormone radioimmunosasay (2nd ed.), pp.657-672, Academic Press, New York and London (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4DD271D6091A3D57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PANCREATIC HORMONE.
                                                                                                                                   59 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00265; PANCREATIC HORMONE 1; 1. PROSITE; PS50276; PANCREATIC HORMONE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro, IPR001955, Pancreatic hormn. Pfam, PF00159, hormone3; 1. ProDom, PD001267; Pancreatic hormu; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 KRHKEDTLAFSEWGSPHAAVPR 171
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36
59
59
6698 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOT YET BEEN ELUCIDATED.
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                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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HSSP; P01302; 1BBA
                                                                                                                                                                                                                                                                     Ovis aries (Sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 40-59.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 AA;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-36.
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9940;
    118 LGK 120
                                          95 AAR 97
                                                                                                                                 PAHO SHEEP
P01301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD RES
NON TER
SEQUENCE
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                                                                                                                 PAHO_SHEEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lbb-sib.ch).
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                                                                                                                                                                                                                                                                                                  EQUENCE FROM N.A.

KDLINE=89104395; PubMed=1214179;

KOPIN A.S., TOGER A.E., Leiter A.B.;

KOPIN A.S., TOGER A.E., Leiter A.B.;

Liferent splice site utilization generates diversity between the rat and human pancreatic polypeptide precursors.";

LL Sinchem. BlobMys. 26:742-748(1988).

-1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS

OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND GASTROLIVESTIVAL FUNCTIONS.

-1- SUBCELDULAR LOCATION: Secreted.

-1- SUBCELDULAR LOCATION: Secreted.

-1- DOMAIN: IN RAT PRECURSOR, THE PEPTIDE WHICH IS FOUND AT THE C-TERMINAL OF PANCREATIC HORMONE DOES NOT SHOW ANY HOWOLOGY TO PANCREATIC ISOCAPEPTIDE WHICH IS FOUND AT THE C-TERMINAL OF THE PRECURSOR OF HUMAN PANCREATIC HORMONE.

CHARACTERISTIC ISOCAPEPTIDE WHICH IS FOUND AT THE C-TERMINAL OF THE PRECURSOR OF HUMAN PANCREATIC HORMONE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRPRCVPQLGREIPAPGTLGPLHIPGHTLSPAPAPAPARALGKTGHLCST---GLDQCA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 236.5; DB 1; Length 98;
Pred. No. 7.8e-12;
6; Mismatches 27; Indels 29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MAVAYYCLSLFLLSTWVALLLQPLQGAWGAPLEPMYPGDYATHEQRAQYETQLRRYINTL 60
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PROSITE; PSS0276; PANCREATIC_HORMONE_2; 1.
HORMOne; Amidation; Pancreas; Cleavage on pair of basic residues;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (G-66 PROVIDE AMIDE GROUP)
                                                                                                                                                                                                                                 "Mosaic evolution of prepropancreatic polypeptide. II. Structural
                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=88139354; PubMed=3343236;
Yonekura H., Nata K., Watanabe T., Kurashina Y., Yamamoto H.,
                                                                                                                                                                                                                                               conservation and divergence in pancreatic polypeptide gene.". J. Biol. Chem. 263:2990-2997(1988).
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                                                        MEDLINE-86196026; PubMed=3009446;
Yanamanco H., Nata K., Okamotco H.;
Mosaic evolution of prepropancreatic polypeptide.";
J. Biol. Chem. 261:6156-6159(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PANCREATIC HORMONE.
C-TERMINAL PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P01302; 1BBA.
InterPro; IPR001955; Pancreatic_hormn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00278; PANCHORMONE. SMART; SMO0309; PAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10975 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M13588; AAA41923.1; -.
EMBL; M18207; AAA41922.1; -.
EMBL; M27450; AAA99236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 24.5%;
1 Similarity 49.6%;
61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29
65
98
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PIR; S06472; S06472.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98 AA;
                                          SEQUENCE FROM N.A.
NCEL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDE
PEPTIDE
MOD_RES
SEQUENCE
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chemical assay.";

Peptides 11:693-685(1990).

Chemical assay.";

Peptides 11:693-685(1990).

Chemical assay.";

Chemical assay
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Mammalia, Eutheria, Rodentia, Hystricognathi, Chinchillidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Pancreas;
MEDLINE=91045327; PubMed=2235678;
BDJ J., Kleinman W.A., Chu L.S.,
"Purification of peptide hormones from chinchilla pancreas by
     LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
                                                                                                                                                                                                                                                                                                                                                                                                                   18.9%; Score 182; DB 1; Length 36; 97.1%; Pred. No. 4.3e-08; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 180; DB 1; Length 36;
Pred. No. 6.1e-08;
2; Mismatches 0; Indels
                             GASTROINTESTINAL FUNCTIONS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                   761B717671A6308F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES 36 36 AMIDATION.
SEQUENCE 36 AA; 4215 MW; 761B717670E3308F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone (Pancreatic polypeptide) (PP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 APLEPVYPGDNATPEQMAQYAAELRRYINMLTRPR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
                                                                                                        HSSP, P01302, 1BBA.

InterPro, 1PR001955, Pancreatic_hormn.

Pfan, PF00159, hormone3; 1.

PRINTS, PR00278, PANCHORMONE.

SMART; SM00309, PAH; 1.

PROSITE; PS00265; PANCREATIC HORMONE 1; 1.

PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR
                                                                                                                                                                                                                                                                                                                                     AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chinchilla brevicaudata (Chinchilla).
                                                                                                                                                                                                                                                                                                       Hormone, Amidation, Pancreas.
MOD_RES 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone, Amidation, Pancreas.
MOD_RES 36
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 36 AA; 4197 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chinchilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHIBR
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P41519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAHO CHIBR
ID PAHO C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yu J., Xin Y., Eng J., Yalow R.S.; "Rhesus monkey gastroenteropancreatic hormones: relationship to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND GASTROINTESTINAL FUNCTIONS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE NPY / PPY FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92225314; PubMed=1808025; Hepry J.S., Lance V.A., Conlon J.M.; Hepry J.S., Lance V.A., Conlon J.M.; Primary structure of pancreatic polypeptide from four species of Perisodactyla (Przewalski's horse, zebra, rhino, tapir)."; Gen. Comp. Endocrinol. 84:440-446(1991).
-i- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Tapiridae, Tapirus.
NCBI TaxID=30582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19.3%; Score 186; DB 1; Length 36; 100.0%; Pred. No. 2.1e-08; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36 36 AMIDATION.
36 AA; 4183 MW; 761B717671A7758F CRC64;
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01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone (Pancreatic polypeptide) (PP).
                                                                                                                                                                                                                                                                                                             Pancreatic hormone (Pancreatic polypeptide) (PP)
                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSO0265; PANCREATIC HORMONE 1; 1.
PROSITE; PS50276; PANCREATIC HORMONE 2; 1.
PAUGINE; Pancreas; Amidation.
MOD. RES.
MOD. RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001955; Pancreatic hormn.
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                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tapirus pinchaque (Mountain tapir)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE.
MEDLINE=91164506; PubMed=2003150;
                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta (Rhesus macaque).
38 KDKEGTLDFLECGSPHSAVPR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFam; PF00159; hormone3; 1.
PRINTS; PR00278; PANCHORMONE.
SMART; SM00309; PAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regul. Pept. 32:39-45(1991)
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                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithécinae; Macaca.
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HSSP; P01302; 1BBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI TaxID=9544;
                                                                                                                                                                       PAHO MACMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAPPI
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P39659;
                                                                                                              RESULT 9
PAHO_MACMU
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Henry J.S., Lance V.A., Conjon J.M.;
Henry J.S., Lance V.A., Conjon J.M.;
Henry J.S., Lance V.A., Conjon J.M.;
Primary structure of pancreatic polypeptide from four species of
Primary structure of pancreatic polypeptide from four species of
Primary structure of pancreatic polypeptide from four species of
GPL Subdocklands in Acrs As A REGULATOR OF PANCREATIC AND
GASTROINTESTINAL FUNCTION: Secreted.

-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIBLIARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
PIR; B61132; B61132.
RISSP, P01302; 1BBA.
RISSP, P01302; BANCHORNONE.
RRSP, PR00195; PANCHORNONE.
RRINTS; PR00278; PANCHORNONE.
RRSMART; SM00309; PAH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Perissodactyla, Rhinocerotidae, Ceratotherium.
NCBI_TaxID=9807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 176; DB 1; Length 36; Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                    Score 177; DB 1; Length 36;
                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o; Indels
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36 AA; 4214 MW; 761B716F8CE2908F CRC64;
                                                                                                                                                                                                                               AMIDATION.
7611D1DC71A6308F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pancreatic hormone (Pancreatic polypeptide) (PP).
                                                                                                                                                                                                                                                                                                                                                  le-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                               18.4%; Sco. No. 10.94.3%; Pred. No. 10. 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 APLEPUYPGDDATPEQMAQYAAELRRYINMLTRPR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
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(Rel. 31, Last sequence update)
                     InterPro; IPR001955; Pancreatic_hormn.
PFUNTS; PR00289; PANCHORMONE.
BRART; SM00309; PAH; 1.
PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
PROSITE; PS00276; PANCREATIC_HORMONE_2; 1.
HORMONE, Amidation; Pancreas, 346
36 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Mismatches
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PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
Hormone; Amidation; Pancreas.
MOD RS AMIDATION
SEQÜENCE 36 AA; 4214 WW; 761B716F8CE29(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92225314; PubMed=1808025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1994 (Rel. 30, Created)
01-FEB-1995 (Rel. 31, Last seq
16-0CT-2001 (Rel. 40, Last anno
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Best Local Similarity 91.4%;
Matches 32; Conservative
                                                                                                                                                                                                                                                          36 AA; 4198 MW;
                                                                                                                                                                                                                                                                                                                                                                          33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
            HSSP; P01302; 1BBA
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAHO ERIEU
P41335;
01-FEB-1995 (
01-FEB-1995 (
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                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                    Query Match
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PAHO_ERIEU
                                                                                                                                                                                                                                                                                                                                                                             Matches
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PT
DT
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                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
GASTROINTESTINAL FUNCTIONS.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: BELONGS TO THE NPY / PPY / PYY FAMILY.
PIR; A01568; PCPG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                    Eguus zebra (Mountain zebra), and
Eguus caballus przewalskii (Przewalski's horse).
Eukaryota; Metazoa; Chordaca; Craniaca; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Eguidae; Eguus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ٥;
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(In) Baba S., Kaneko T., Yanaihara N. (eds.);
Proinsulin, insulin, c-peptide, pp.419-425, Excerpta Medica,
Amsterdam (1979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 180; DB 1; Length 36;
Pred. No. 6.1e-08;
2; Mismatches 0; Indels
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                                                                              01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone (Pancreatic polypeptide) (PP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
Pancreatic hormone (Pancreatic polypeptide) (PP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A61132; A61132.

PIR; D61132; D61132.

HSSP: P011020; 1BBA.

InterPro; 1BR001955; Pancreatic_hormn.

Pfam; PF00159; hormone3; 1.

PRINTS; PR00278; PANCREMONE.

PROSITE; PS00265; PANCREATIC_HORMONE 1; 1.

PROSITE; PS0276; PANCREATIC_HORMONE 2; 1.

HORMONE; Amidation; Pancreas.

MOD RES 36 36 36 36 36 SEQÜENCE 36 AA; 4215 MW; 761ADA6CC1A6308F
                                 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 APLEPVYPGDNATPEQMAQYAADLRRYINMLTRPR 64
                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 94.3%;
Matches 33; Conservative
                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                 EQUZE
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P01300;
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PAHO COUZE ID PAHO E
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